

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:56:10 ; Search time 10.25 Seconds
(without alignments)
112.614 Million cell updates/sec

Title: US-09-730-174A-3
Perfect score: 59
Sequence: 1 SVSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1561

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------------|---------------------|
| 1 | 21 | 35.6 | 12 2 S21205 | Ig heavy chain V r |
| 2 | 18 | 30.5 | 7 2 A58718 | carnocin UT49 - Ca |
| 3 | 18 | 30.5 | 9 2 S78420 | ribosomal protein |
| 4 | 18 | 30.5 | 10 2 A60589 | sperm-activating p |
| 5 | 18 | 30.5 | 10 2 B46453 | e antigen p20e pre |
| 6 | 17 | 28.8 | 7 2 I46868 | alpha-myosin heavy |
| 7 | 17 | 28.8 | 10 2 S28055 | cytochrome b559 co |
| 8 | 17 | 28.8 | 10 2 A37268 | Ig heavy chain C r |
| 9 | 16 | 27.1 | 9 2 S13636 | coat protein beta |
| 10 | 16 | 27.1 | 10 2 A47364 | placental lactogen |
| 11 | 15 | 25.4 | 7 2 S25266 | pil protein - Bsc |
| 12 | 15 | 25.4 | 7 2 S29735 | polyposphatase-glu |
| 13 | 15 | 25.4 | 9 2 PM0002 | chlorophyll a/b-b1 |
| 14 | 15 | 25.4 | 9 2 A56029 | N-methylpurine DNA |
| 15 | 15 | 25.4 | 10 2 S27873 | hypothetical prote |
| 16 | 15 | 25.4 | 11 2 A38841 | rhodopsin homolog |
| 17 | 15 | 25.4 | 11 2 S35490 | type II site-speci |
| 18 | 15 | 25.4 | 11 2 B41835 | translation elonga |
| 19 | 15 | 25.4 | 11 2 A40795 | glycoprotein H-a - |
| 20 | 15 | 25.4 | 12 2 A55837 | 5-aminimidazole r |
| 21 | 14 | 23.7 | 4 2 I38888 | COI intron 16 prot |
| 22 | 14 | 23.7 | 7 2 JN0859 | peptidyl-dipectida |
| 23 | 14 | 23.7 | 7 2 T09512 | NADH2 dehydrogenas |
| 24 | 14 | 23.7 | 9 2 PT0238 | Ig heavy chain CRD |
| 25 | 14 | 23.7 | 10 1 SPGNK | neutomedin K - pig |
| 26 | 14 | 23.7 | 10 2 C61033 | ranatachykinin C - |
| 27 | 14 | 23.7 | 11 2 A55149 | tetracenomycin A2 |
| 28 | 14 | 23.7 | 11 2 S60354 | retinal oxidase - |
| 29 | 14 | 23.7 | 11 2 B29806 | acidic proline-rich |

| | | | | |
|----|----|------|-------------|--------------------|
| 30 | 14 | 23.7 | 11 2 PH0904 | T-cell receptor be |
| 31 | 14 | 23.7 | 11 2 PH0924 | T-cell receptor be |
| 32 | 14 | 23.7 | 11 4 S41909 | hypothetical prote |
| 33 | 14 | 23.7 | 12 2 S25485 | transcription fact |
| 34 | 14 | 23.7 | 12 2 G49410 | t-complex polypept |
| 35 | 14 | 23.7 | 12 2 S71034 | poB protein - Sal |
| 36 | 14 | 23.7 | 12 2 C60529 | hemocyanin I - gre |
| 37 | 14 | 23.7 | 12 2 PH1190 | T-cell receptor al |
| 38 | 14 | 23.7 | 12 2 PH1187 | T-cell receptor al |
| 39 | 14 | 23.7 | 12 2 PH1189 | T-cell receptor al |
| 40 | 14 | 23.7 | 12 2 I41235 | glutamine-tRNA lig |
| 41 | 13 | 22.0 | 6 2 A20186 | fatty-acid synthas |
| 42 | 13 | 22.0 | 8 2 T14905 | hypothetical prote |
| 43 | 13 | 22.0 | 8 2 JS0316 | leucokinin VI - Ma |
| 44 | 13 | 22.0 | 8 2 PH1618 | Ig H chain V-D-U r |
| 45 | 13 | 22.0 | 9 2 JN0026 | sperm-activating p |

ALIGNMENTS

RESULT 1

S21205
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #ext_change 16-Aug-1996
C:Accession: S21205
R:Makiya, R., Strigand, T.
Eur. J. Biochem. 205, 341-345, 1992
A:Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin
A:Reference number: S21205; M01D:92209522; PM1D:1555592
A:Accession: S21205
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <MA>
C:Keywords: heterotetramer; immunoglobulin

Query Match 35.6% ; Score 21; DB 2; Length 12;
Best Local Similarity 44.4% ; Pred. No. 6.5e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 EIQLMHNLG 12
DB 1 EVQLVESGG 9

RESULT 2

A58718
carnocin UT49 - Carnobacterium sp. (fragment)
C:Species: Carnobacterium sp.
C>Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #ext_change 30-Jan-1998
R:Stoefels, G., Missen-Ney, J., Gudmundsdottir, A., Sletten, K., Hojo, H., Nes, I.F.
Appl. Environ. Microbiol. 58, 1417-1422, 1992
A:Title: Purification and characterization of a new bacteriocin isolated from a Carnobac
A:Reference number: A58718; M01D:92321768; PM1D:1622206
A:Accession: A58718
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <STO>
C:Keywords: antibiotic; lanthionine

Query Match 30.8% ; Score 18; DB 2; Length 7;
Best Local Similarity 100.0% ; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6
DB 2 SEIQ 5

RESULT 3

S78420

ribosomal protein RL41, mitochondrial [validated] - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000

C/Accession: S78420

R/Goldschmidt-Reisin, S.; Grack, H.R. submitted to the Protein Sequence Database, February 1998

A/Reference number: S78411

A/Accession: S78420

A/Molecule type: protein

A/Residues: 1-9 <GOL>

A/Note: the protein is designated as mitochondrial ribosomal protein L41

C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match

Best Local Similarity 30.5%; Score 18; DB 2; Length 9;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12

DB 5 HRLG 8

RESULT 4

A60589

sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchin

C/Species: Heterocentrotus mamillatus

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000

C/Accession: A60589

R/Toshino, K.I.; Kajimura, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi, K.

Comp. Biochem. Physiol. B 94, 739-751, 1989

A/Title: A halogenated amino acid-containing sperm activating peptide and its related peptides

A/Reference number: A60527

A/Accession: A60589

A/Molecule type: protein

A/Residues: 1-10 <TOS>

C/Superfamily: unassigned animal peptides

Query Match

Best Local Similarity 30.5%; Score 18; DB 2; Length 10;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNLG 12

DB 2 YNLG 5

RESULT 5

B46453

e antigen p20e precursor - hepatitis B virus (subtype adr) (fragment)

N/Alternate names: HBe antigen precursor

N/Contains: e antigen

C/Species: hepatitis B virus, HBV

C/Date: 18-Jun-1993 #sequence_revision 08-Nov-1996 #text_change 15-Aug-1997

DB

1 MOLFM 5

RESULT 6

146868

alpha-myosin heavy chain - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999

C/Accession: I46868

R/Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.

Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984

A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula

A/Reference number: I46868; MUID:84221901; PMID:6328491

A/Accession: I46868

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-7 <FR1>

A/Cross-references: GB:K01698; NID:G165538; PID:AAA31415.1; PID:G165539

Query Match

Best Local Similarity 28.8%; Score 17; DB 2; Length 7;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QLMNH 10

DB 1 QKMH 5

RESULT 7

S28055

cytochrome b559 component psbf - pepper chloroplast (fragment)

C/Species: chloroplast Capsicum annuum (pepper)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jun-1999

C/Accession: S28055

R/Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.

Plant Mol. Biol. 20, 1185-1186, 1992

A/Title: The psbf gene from bell pepper (Capsicum annuum): plastid RNA editing also occurs

A/Reference number: S28055; MUID:93099270; PMID:1463853

A/Accession: S28055

A/Molecule type: DNA

A/Residues: 1-10 <KUN>

A/Cross-references: EMBL:X65570; NID:G14344; PID:CAA46539.1; PID:G145724

C/Genetics:

A/Gene: psbf

A/Genome: chloroplast

C/Superfamily: cytochrome b559 component F

C/Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

DB

1 SVSEIOLM 8

RESULT 8

A37268

heavy chain C region (129) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998

C/Accession: A37268

R/Kuff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A/Title: Heavy and light chain variable region sequences and antibody properties of anti

A/Reference number: A38740; MUID:91177923; PMID:1706720

A/Accession: A37268

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-10 <RUF>

Query Match

Best Local Similarity 28.8%; Score 17; DB 2; Length 10;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIOLM 8

DB 1 SISAMQFI 8

RESULT 9

A37268

heavy chain C region (129) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998

C/Accession: A37268

R/Kuff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A/Title: Heavy and light chain variable region sequences and antibody properties of anti

A/Reference number: A38740; MUID:91177923; PMID:1706720

A/Accession: A37268

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-10 <RUF>

Query Match

Best Local Similarity 28.8%; Score 17; DB 2; Length 10;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIOLM 8

DB 1 SISAMQFI 8

RESULT 10

A37268

DB

1 MOLFM 5

RESULT 6

146868

alpha-myosin heavy chain - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999

C/Accession: I46868

R/Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.

Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984

A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula

A/Reference number: I46868; MUID:84221901; PMID:6328491

A/Accession: I46868

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-7 <FR1>

A/Cross-references: GB:K01698; NID:G165538; PID:AAA31415.1; PID:G165539

Query Match

Best Local Similarity 28.8%; Score 17; DB 2; Length 7;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QLMNH 10

DB 1 QKMH 5

RESULT 7

S28055

cytochrome b559 component psbf - pepper chloroplast (fragment)

C/Species: chloroplast Capsicum annuum (pepper)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jun-1999

C/Accession: S28055

R/Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.

Plant Mol. Biol. 20, 1185-1186, 1992

A/Title: The psbf gene from bell pepper (Capsicum annuum): plastid RNA editing also occurs

A/Reference number: S28055; MUID:93099270; PMID:1463853

A/Accession: S28055

A/Molecule type: DNA

A/Residues: 1-10 <KUN>

A/Cross-references: EMBL:X65570; NID:G14344; PID:CAA46539.1; PID:G145724

C/Genetics:

A/Gene: psbf

A/Genome: chloroplast

C/Superfamily: cytochrome b559 component F

C/Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

DB

1 SVSEIOLM 8

RESULT 8

A37268

heavy chain C region (129) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998

C/Accession: A37268

R/Kuff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A/Title: Heavy and light chain variable region sequences and antibody properties of anti

A/Reference number: A38740; MUID:91177923; PMID:1706720

A/Accession: A37268

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-10 <RUF>

Query Match

Best Local Similarity 28.8%; Score 17; DB 2; Length 10;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIOLM 8

DB 1 SISAMQFI 8

RESULT 9

A37268

heavy chain C region (129) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998

C/Accession: A37268

R/Kuff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A/Title: Heavy and light chain variable region sequences and antibody properties of anti

A/Reference number: A38740; MUID:91177923; PMID:1706720

A/Accession: A37268

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-10 <RUF>

Query Match

Best Local Similarity 28.8%; Score 17; DB 2; Length 10;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIOLM 8

DB 1 SISAMQFI 8

RESULT 10

A37268

Query Match 28.8%; Score 17; DB 2; Length 10;
 Best Local Similarity 44.4%; Pred. No. 3.1e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EICLMHNG 12
 |||
 |||
 Db 1 ESQSPFNVG 9

RESULT 9
 S13636
 coat protein beta chain, Golgi-derived - rabbit (fragment)
 N/Alternate names: beta-COP protein
 C/Species: *Oryctolagus cuniculus* (domestic rabbit)
 C/Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
 C/Accession: S13636
 R/Serafini, T.; Stenbeck, G.; Brecht, A.; Lottspeich, F.; Orci, L.; Rothman, J.E.; Wieda
 Nature 349, 215-220, 1991
 A/Title: A coat subunit of Golgi-derived non-clathrin-coated vesicles with homology to t
 A/Reference number: S13636; PMID:91101693; PMID:1898984
 A/Accession: S13636
 A/Molecule type: protein
 A/Residues: 1-9 <SER>
 A/Superfamily: coarctomer complex beta chain
 C/Keywords: Golgi apparatus; protein transport

Query Match 27.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 37.5%; Pred. No. 2.8e+05;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIQLM 8
 |||
 |||
 Db 1 STGEIPIV 8

RESULT 10
 A47364
 placental lactogen-1 precursor - mouse (fragment)
 C/Species: *Mus sp.* (mouse)
 C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
 C/Accession: A47364
 R/Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.
 Mol. Endocrinol. 7, 181-188, 1993
 A/Title: Trophoblast-specific transcription from the mouse placental lactogen-1 gene pro
 A/Reference number: A47364; PMID:9325959; PMID:8469232
 A/Accession: A47364
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-10 <RES>
 A/Cross-references: GB:S58124; NID:G299449

Query Match 27.1%; Score 16; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 4.9e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IQLMNL 11
 |||
 |||
 Db 1 MQTLNL 7

RESULT 11
 S25266
 p115 protein - *Escherichia coli* (fragment)
 C/Species: *Escherichia coli*
 C/Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 11-Jun-1993
 C/Accession: S25266
 R/Dupuy, B.; Tah, M.K.; Posso, O.; Marchal, C.; Pugsley, A.P.
 Mol. Microbiol. 6, 1887-1894, 1992
 A/Title: P115, a component of the pullulanase secretion pathway of *Klebsiella oxytoca*, c
 A/Reference number: S25266; PMID:92374839; PMID:1354833
 A/Accession: S25266
 A/Molecule type: protein
 A/Residues: 1-7 <DUP>

C/Genetics:
 A/Genes: p115

Query Match 25.4%; Score 15; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQLM 8
 |||
 |||
 Db 4 IEIM 7

RESULT 12
 S29735
 polyphosphate-glucose phosphotransferase (EC 2.7.1.63) - *Propionibacterium freudenreichi*
 C/Species: *Propionibacterium freudenreichi* subsp. *shermanii*
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
 C/Accession: S29735
 R/Phillips, N.F.B.; Horn, P.J.; Wood, H.G.
 Arch. Biochem. Biophys. 300, 309-319, 1993
 A/Title: The polyphosphate- and ATP-dependent glucokinase from *Propionibacterium shermani*
 A/Reference number: S29735; PMID:93143332; PMID:8380966
 A/Accession: S29735
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-7 <PHI>
 C/Keywords: phosphotransferase

Query Match 25.4%; Score 15; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12
 |||
 |||
 Db 2 HTLG 5

RESULT 13
 P00002
 chlorophyll a/b-binding protein 31k - green alga (*Dunaliella tertiolecta*) (fragment)
 N/Alternate names: photosystem II light-harvesting chlorophyll 31k protein
 C/Species: *Dunaliella tertiolecta*
 C/Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
 C/Accession: P00002
 R/Laroche, J.; Bennett, J.; Falkowski, P.G.
 Gene 95, 165-171, 1990
 A/Title: Characterization of a cDNA encoding for the 28.5-kDa LHClI apoprotein from the
 A/Reference number: U00040; PMID:9105528; PMID:2249775
 A/Accession: P00002
 A/Molecule type: protein
 A/Residues: 1-9 <LAR>
 C/Superfamily: chlorophyll a/b-binding protein
 C/Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane pr

Query Match 25.4%; Score 15; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 EIQLM 8
 |||
 |||
 Db 5 EMQAM 9

RESULT 14
 A56029
 N-methylpurine DNA glycosylase - mouse (fragment)
 C/Species: *Mus musculus* (house mouse)
 C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 19-Jan-1996
 C/Accession: A56029
 R/Roy, R.; Brooks, C.; Mitra, S.
 Biochemistry 33, 15131-15140, 1994
 A/Title: Purification and biochemical characterization of recombinant N-methylpurine-DNA
 A/Reference number: A56029; PMID:95092772; PMID:7999773

A:Accession: A56029
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-9 <ROY>

Query Match 25.4%; Score 15; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12
|||
3 HEVG 6

RESULT 15

S27873
hypothetical protein 2 LRH-1 5'-region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C/Accession: S27873
R/Tugwood, J.D.; Isseman, I.; Green, S.
submitted to the EMBL Data Library, February 1992
A:Description: LRH-1: A nuclear hormone receptor active in the absence of exogenous ligand
A:Reference number: S27873
A:Accession: S27873
A:Molecule type: mRNA
A:Residues: 1-10 <TUG>
A:Cross-references: EMBL:M81385; NID:G198872; PIDN:AAA39446.1; PID:G198874
C:Superfamily: unassigned leader peptides

Query Match 25.4%; Score 15; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQ 6
|||
Db 5 NLSTIQ 10

Search completed: May 18, 2004, 10:05:40
Job time : 11.25 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:43:45 ; Search time 6.75 seconds

(without alignments)

92.569 Million cell updates/sec

Title: US-09-730-174a-3

Perfect score: 59

Sequence: 1 SVSEIQLMHNIG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | ID | Description |
|------------|-------|---------------|--------|----|-------------|
| 1 | 18 | 30.5 | 7 | 1 | LANC CARUI |
| 2 | 17 | 28.8 | 10 | 1 | PSBF_CAPAN |
| 3 | 16 | 27.1 | 8 | 1 | ALB6_CYDPO |
| 4 | 16 | 27.1 | 8 | 1 | FUSS_FUSSO |
| 5 | 16 | 27.1 | 10 | 1 | RRLP_PHOBY |
| 6 | 16 | 27.1 | 11 | 1 | ERG_GLOPA |
| 7 | 15 | 25.4 | 11 | 1 | PVKI_PERRM |
| 8 | 15 | 25.4 | 11 | 1 | TRP1_PEROY |
| 9 | 14 | 23.7 | 7 | 1 | TRP1_PSEBU |
| 10 | 14 | 23.7 | 7 | 1 | ALB7_CYDPO |
| 11 | 14 | 23.7 | 8 | 1 | ALB8_CARMA |
| 12 | 14 | 23.7 | 9 | 1 | ALB1_CYDPO |
| 13 | 14 | 23.7 | 9 | 1 | FAR8_MACRS |
| 14 | 14 | 23.7 | 9 | 1 | UF02_MOUSE |
| 15 | 14 | 23.7 | 10 | 1 | ALB9_CARMA |
| 16 | 14 | 23.7 | 10 | 1 | ALB10_CARMA |
| 17 | 14 | 23.7 | 10 | 1 | TRNK_RANCA |
| 18 | 14 | 23.7 | 10 | 1 | TRNK_PIG |
| 19 | 14 | 23.7 | 11 | 1 | ASL1_BACSE |
| 20 | 14 | 23.7 | 12 | 1 | CDI4_LITXA |
| 21 | 14 | 23.7 | 12 | 1 | CDI4_LITXA |
| 22 | 14 | 23.7 | 12 | 1 | HCY1_CARMA |
| 23 | 14 | 23.7 | 12 | 1 | FOR1_METTM |
| 24 | 14 | 23.7 | 12 | 1 | RS19_TOBBP |
| 25 | 13 | 22.0 | 8 | 1 | LCK4_LEUMA |
| 26 | 13 | 22.0 | 8 | 1 | LCK6_LEUMA |
| 27 | 13 | 22.0 | 9 | 1 | MOSH_CLYUA |
| 28 | 13 | 22.0 | 9 | 1 | PKP1_PERRM |
| 29 | 13 | 22.0 | 11 | 1 | CS15_BACSU |
| 30 | 13 | 22.0 | 11 | 1 | OZ0A_COMTE |
| 31 | 13 | 22.0 | 12 | 1 | PA2B_VIPRO |
| 32 | 13 | 22.0 | 12 | 1 | PKP4_PERRM |
| 33 | 13 | 22.0 | 12 | 1 | UR2_POLSP |

| | | | | | |
|----|----|------|----|---|--------------------|
| 34 | 12 | 20.3 | 9 | 1 | FIBB_PAPHA |
| 35 | 12 | 20.3 | 9 | 1 | RE42_LITRU |
| 36 | 12 | 20.3 | 10 | 1 | GLEW_HUMAN |
| 37 | 12 | 20.3 | 10 | 1 | GONI_CLYUA |
| 38 | 12 | 20.3 | 10 | 1 | GON2_CHEPR |
| 39 | 12 | 20.3 | 10 | 1 | HTP1_ROMMT |
| 40 | 12 | 20.3 | 10 | 1 | HTP1_HEIZE |
| 41 | 12 | 20.3 | 10 | 1 | SYK_CAMUP |
| 42 | 12 | 20.3 | 10 | 1 | TKNB_RANRI |
| 43 | 12 | 20.3 | 11 | 1 | CSX1_CONMR |
| 44 | 12 | 20.3 | 11 | 1 | HS70_PINPS |
| 45 | 12 | 20.3 | 12 | 1 | HEP1_BACSE |
| | | | | | P19343 papio hamad |
| | | | | | P82075 litoria rub |
| | | | | | P02728 homo sapien |
| | | | | | P81749 clupea pall |
| | | | | | P80678 chelyosoma |
| | | | | | P18110 romalea mic |
| | | | | | P16353 heliothis z |
| | | | | | Q46464 campylobact |
| | | | | | P29135 rana ridibu |
| | | | | | P58807 conus marmo |
| | | | | | P81672 pinus pinas |
| | | | | | P83054 bacteroides |

ALIGNMENTS

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RESULT 1
ID LANC CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin U149 (Fragment).
OS Carnobacterium sp. (strain U149).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Weyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).
CC Active on Gram-positive bacteria.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON_TER
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 30.5%; Score 18; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEQ 6
DB 2 SETQ 5

RESULT 2
ID PSBF CAPAN STANDARD; PRT; 10 AA.
AC Q03367;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI)
DE (Fragment).
OS PSBF.
OS Capsicum annuum (Bell pepper).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;
RX MEDLINE=9309270; PubMed=1463853;
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;

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RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA
RT editing also occurs in non-photosynthetic chromoplasts.";
RL Plant Mol. Biol. 20:1185-1188(1992).
CC -1- FUNCTION: This b-type cytochrome is tightly associated with the
CC reaction center of photosystem II and possibly is part of the
CC water-oxidation complex.
CC -1- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC -1- SIMILARITY: Belongs to the psbD / psbF family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X6570; CAA46539.1; -.
CC PIR: S28055; S28055.
DR HAMAP: MF_00643; -; 1.
DR InterPro: IPR006216; GYC_B559.
DR PROSITE: PS00537; CYTOCHROME_B559; PARTIAL.
DR Chloplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT NON TER 1 1
FT TRANSMEM <1 5
FT DOMAIN 6 10 BY SIMILARITY.
FT SEQUENCE 10 AA; 1180 MW; 817D0F59D6D9DC5 CRC64;

Query Match 28.8%; Score 17; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.9e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 SVSEIQLM 8
Db 1 SISAMOFI 8

RESULT 3

AL16 CYDPO STANDARD; PRT; 8 AA.
ID ALL6 CYDPO
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 6.
OS Cydia pomonella (codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allostatin family.
CC KW Neuropeptide; Amidation.
FT MOD RES 8
FT SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 27.1%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 8 MENTLG 12
Db 3 LYNFG 7

RESULT 4

FUSO_FUSO STANDARD; PRT; 8 AA.
ID FUSO_FUSO
AC P61010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Allergen Fus s. 13596* (Fragment).
OS Ficus solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=LARI 3596; Tissue=Mycelium;
RA Verma J., Gangai S.V.;
RL Submitted (JUL-1997) to Swiss-Prot.
CC -1- ALLERGEN: Causes an allergic reaction in human.
KW Allergen.
FT NON TER 8
FT SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 27.1%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 LMENL 11
Db 3 MSHNV 7

RESULT 5

RRPL PHODV STANDARD; PRT; 10 AA.
ID RRPL PHODV
AC P35916;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.46) (large structural protein)
DE L. protein (Fragment).
GN L.
OS Phocine distemper virus (PDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Juster/88;
RX MEDLINE=92266877; PubMed=1568321;
RA Curran M.D., O'Loon D., Kennedy S., Rima B.K.;
RT "Molecular characterization of phocine distemper virus: gene order
RT and sequence of the gene encoding the attachment (H) protein.";
RL J. Gen. Virol. 73:1189-1194(1992).
CC -1- FUNCTION: Probable component of the active polymerase. It may
CC function in mRNA synthesis, capping, methylation and poly(A)
CC synthesis of newly synthesized viral mRNAs. RNA editing of the P
CC gene transcript, and protein kinase activity.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA) (N).
CC -----
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CC -----
CC EMBL: D10371; BAA01208.1; -.
DR Transferase; RNA-directed RNA polymerase.
FT NON TER 10 10
FT SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;

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Query Match      27.1%; Score 16; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 SVSEIQLM 8
      ||| |||
      3 SVSVNQLL 10

RESULT 6
EFG_CLOPA
AC EFG_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OK NCBI_TaxID=1501;
RN (1)
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Pflieger R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of
the nascent protein chain from the A-site to the P-site of the
ribosome.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACITOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON TER 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C3B17 CRC64;

Query Match      27.1%; Score 16; DB 1; Length 11;
Best Local Similarity 25.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      5 IOLMENIG 12
      ||| |||
      4 LEKFORIG 11

RESULT 7
PVK1_PERAM
ID PVK1_PERAM STANDARD; PRT; 11 AA.
AC P41837;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-1 (Pee-PVK-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OK NCBI_TaxID=6978;
RN (1)
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=9532021; PubMed=7716075;
RA Pregel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT "Periviscerokinin (Pee-PVK): a novel myotropic neuropeptide from the
RT perisymphathetic organs of the American cockroach."
RT Peptides 16:61-66(1995).
-1- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE

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CC HYPERNEURAL MUSCLE.
KW Neuropeptide; Amidation.
FT MOD RES 11
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match      25.4%; Score 15; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      5 IOLMEN 10
      ||| |||
      6 IPVFRN 11

RESULT 8
T2P1_PROVU
ID T2P1_PROVU STANDARD; PRT; 11 AA.
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
DE (R.PvuI) (Fragment).
GN PVUIR.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OK NCBI_TaxID=585;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13115;
RX MEDLINE=93087186; PubMed=1454536;
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvuI restriction and
RT modification system."
RL Nucleic Acids Res. 20:5743-5747(1992).
CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CLEAVES AFTER T-4.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
specific double-stranded fragments with terminal 5'-phosphates.
CC -----
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CC -----
DR EMBL; L04163; AAA25660.1; -
DR PIR; S35490; S35490.
DR REBASE; 1541; PvuI.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
FT NON TER 1
SQ SEQUENCE 11 AA; 1300 MW; 9FC0DE7955B72B1A CRC64;

Query Match      25.4%; Score 15; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 SVSEI 5
      ||| |||
      2 SYDEL 6

RESULT 9
TRP1_PSEPU
ID TRP1_PSEPU STANDARD; PRT; 6 AA.
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE HTH-type transcriptional regulator trpI (trpBA operon transcriptional

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DE activator) (Fragment).
 GN TRPI.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 (1)
 RN SEQUENCE FROM N.A.
 RP STRAIN=PGI C18;
 RX MEDLINE=8935826; PubMed=2503057;
 RA Eberly L., Crawford I.P.,
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
 putida";
 RL Biochimie 71:521-531(1989).
 CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPA GENES ENCODING
 THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
 INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
 TRPA OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 CC -1- SIMILARITY: Contains 1 HTH LysR-type DNA-binding domain.
 CC -----
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 CC -----
 DR EMBL; X13299; CAA31660.1; -
 DR InterPro; IPR000847; HTH_LYSR.
 DR PROSITE; PS50931; HTH_LYSR; PARTIAL.
 KM Tryptophan biosynthesis; Transcription regulation; Activator;
 KM DNA-binding.
 FT NON_TER
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F00 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMENL 11
 : : :
 Db 1 MAHDL 5

RESULT 10
 ALL7_CYPDPO STANDARD; PRT; 7 AA.
 ID ALL7_CYPDPO
 AC P82158;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 7
 OS Cydia pomonella (Coddling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.,
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 CC
 KM Neuropeptide; Amidation.
 FT MOD_RES
 SQ SEQUENCE 7 AA; 873 MW; 672879CAB569350 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 7;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MNLG 12
 : : :
 Db 2 MYDFG 6

RESULT 11
 AL18_CARMA STANDARD; PRT; 8 AA.
 ID AL18_CARMA
 AC P81821;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 18.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=9812193; PubMed=9461295;
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.,
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 KM Neuropeptide; Amidation; Multigene family (POTENTIAL).
 FT MOD_RBS
 SQ SEQUENCE 8 AA; 919 MW; C82879D5AB569AB5 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MNLG 12
 : : :
 Db 3 MYDFG 7

RESULT 12
 ALL1_CYPDPO STANDARD; PRT; 8 AA.
 ID ALL1_CYPDPO
 AC P82152;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 1.
 OS Cydia pomonella (Coddling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.,
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 CC
 KM Neuropeptide; Amidation.
 FT MOD_RBS
 SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNUG 12
 Db 4 YNFG 7

RESULT 13

PAR8_MACRS STANDARD: PRT: 9 AA.

ID_FAB8_MACRS
 AC P83281;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide RUP8 (VSHNNFLR-amide).
 OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonidae; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Dysentery;
 RX MEDLINE=21107394; PubMed=1179812;
 RA Sitihinggul P., Sarathongkum W., Longyant S., Panchan N.,
 RA Sitihinggul W., Petson A.;
 RT "Three more novel FMRamide-like neuropeptide sequences from the
 RT eye stalk of the giant freshwater prawn Macrobrachium rosenbergii.",
 RL Peptides 22:191-197(2001).
 CC -1- MASS SPECTROMETRY: MW=1133.8, METHOD=MALDI.
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 DR GO:GO:0007218; P:neuropeptide signaling pathway; IDA.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1133 MW; 845A0729C44441F5 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HN 10
 Db 3 HN 4

RESULT 14

UF02_MOUSE STANDARD: PRT: 9 AA.

ID_UF02_MOUSE
 AC P38610;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95069907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis.",
 RL Electrophoresis 15:735-745(1994).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined PI of this unknown
 CC protein is: 6.0, its MW is: 32 kDa.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1102 MW; 7E73EAB6D051AAB CRC64;

Query Match 23.7%; Score 14; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIQ 6
 Db 4 EIQ 6

RESULT 15

AL19_CARMA STANDARD: PRT: 10 AA.

ID_AL19_CARMA
 AC P81822;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 19.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jarvis P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.",
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 10
 SQ SEQUENCE 10 AA; 1101 MW; 96687CDB569AB1 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 7.2e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 HNUG 12
 Db 5 MYSPG 9

Search completed: May 18, 2004, 10:02:33
 Job time : 7.75 secs

DE 01-MAY-2000 (TREMBLrel. 13, last annotation update)
 DE DYNASTIN 3.
 OS Limodynastes terreareginae (Northern banjo frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RT Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 CC Limodynastinae; Limodynastes.
 NCBI_TaxID=104894;
 RN
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION.
 RA Bradley A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structure of the dynastins from
 the banjo frogs Limodynastes terreareginae, Limodynastes dumerilii and
 Limodynastes terreareginae."
 RL Aust. J. Chem. 46:833-842(1993).
 CC -1- MASS SPECTROMETRY: MM=1236; METHOD=FAB.
 SQ SEQUENCE 12 AA; 1236 MW; 147AA70FD7472724 CRC64;

Query Match 39.0%; Score 23; DB 13; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 LMNLG 12
 DB 6 LNLNLG 11

RESULT 3
 ID P82082 PRELIMINARY; PRT; 8 AA.
 AC P82082;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
 DE DYNASTIN 4.
 OS Limodynastes salmini (Salmi's-striped frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 CC Limodynastinae; Limodynastes.
 NCBI_TaxID=39404;
 RN
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structure of the dynastins from
 Limodynastes salmini and Fletcherin from Limodynastes Fletcheri."
 RL Aust. J. Chem. 46:1235-1244(1993).
 CC -1- MASS SPECTROMETRY: MM=772; METHOD=FAB.
 SQ SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;

Query Match 33.9%; Score 20; DB 13; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06; 1;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMNLG 12
 DB 2 LVSNLG 7

RESULT 4
 ID P82083 PRELIMINARY; PRT; 8 AA.
 AC P82083;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
 DE DYNASTIN 5.
 OS Limodynastes salmini (Salmi's-striped frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 CC Limodynastinae; Limodynastes.
 NCBI_TaxID=39404;
 RN
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structure of the dynastins from
 Limodynastes salmini and Fletcherin from Limodynastes Fletcheri."
 RL Aust. J. Chem. 46:1235-1244(1993).
 CC -1- MASS SPECTROMETRY: MM=772; METHOD=FAB.
 SQ SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;

RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Bradley A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structure of the dynastins from
 Limodynastes salmini and Fletcherin from Limodynastes Fletcheri."
 RL Aust. J. Chem. 46:1235-1244(1993).
 CC -1- MASS SPECTROMETRY: MM=786; METHOD=FAB.
 SQ SEQUENCE 8 AA; 786 MW; 7B58772455B05728 CRC64;

Query Match 33.9%; Score 20; DB 13; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+06; 1;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMNLG 12
 DB 2 LISNLG 7

RESULT 5
 ID P82085 PRELIMINARY; PRT; 12 AA.
 AC P82085;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
 DE DYNASTIN 7.
 OS Limodynastes salmini (Salmi's-striped frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 CC Limodynastinae; Limodynastes.
 NCBI_TaxID=39404;
 RN
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Bradley A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structure of the dynastins from
 Limodynastes salmini and Fletcherin from Limodynastes Fletcheri."
 RL Aust. J. Chem. 46:1235-1244(1993).
 CC -1- MASS SPECTROMETRY: MM=1114; METHOD=FAB.
 SQ SEQUENCE 12 AA; 1114 MW; 3AB5A976CAA72728 CRC64;

Query Match 33.9%; Score 20; DB 13; Length 12;
 Best Local Similarity 66.7%; Pred. No. 4.3e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMNLG 12
 DB 6 LNLNLG 11

RESULT 6
 ID Q34909 PRELIMINARY; PRT; 8 AA.
 AC Q34909;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, last annotation update)
 DE Cytochrome b (Fragment).
 OS Locusta migratoria (Migratory locust).
 CC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
 CC Acrididae; Oedipodinae; Locusta.
 NCBI_TaxID=7004;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88223478; PubMed=2836084;
 RA McCracken A., Unkenbusch I., Gellissen G.;
 RT "Structure of the cloned Locusta migratoria mitochondrial genome:
 restriction mapping and sequence of its ND-1 (URF-1) gene."
 RL Curr. Genet. 11:625-630(1987).
 DR EMBL; X05286; CAA28905.1; -;
 DR GO; GO:0005739; C.mitochondrion; IEA.

KM Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 32.2%; Score 19; DB 8; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSEIQLMH 9
 DB 1 MSYIKLKH 8

RESULT 7
 ID 092766 PRELIMINARY; PRT; 9 AA.

AC 092766;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE Fusion protein (Fragment).

GN F.
 OS Canine distemper virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 OX NCBI_TaxID=11232;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dog #5526/89;
 RA Lieberman H., Harder T., Haas L.;
 RT "Genetic analysis of the central untranslated genome region and the proximal coding part of the F gene of wild-type and vaccine distemper morbilliviruses";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF026237; AAC09167.1; -;
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;

Query Match 32.2%; Score 19; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MEN 10
 DB 1 MEN 3

RESULT 8
 ID 071066 PRELIMINARY; PRT; 9 AA.

AC 071066;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Fusion protein (Fragment).

GN F.
 OS Canine distemper virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 OX NCBI_TaxID=11232;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dog #10757/96;
 RA Lieberman H., Harder T., Haas L.;
 RT "Genetic analysis of the central untranslated genome region and the proximal coding part of the F gene of wild-type and vaccine distemper morbilliviruses";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF026234; AAC09164.1; -;
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;

Query Match 32.2%; Score 19; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MEN 10
 DB 1 MEN 3

RESULT 9
 ID 040659 PRELIMINARY; PRT; 8 AA.

AC 040659;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Alpha-amylase (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoae; Oryza.
 OX NCBI_TaxID=4530;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=1078641; PubMed=2258052;
 RA Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
 RA Rodriguez R.L.;
 RT "Expression and secretion of rice alpha-amylase by saccharomyces cerevisiae";
 RL Gene 94:209-216(1990).
 DR EMBL; M62916; AAA33892.1; -;
 DR Gramene; Q40659; -;
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 948 MW; EBC69444472D6D6 CRC64;

Query Match 30.5%; Score 18; DB 10; Length 8;
 Best Local Similarity 28.6%; Pred. No. 1e+06;
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOLMHL 11
 DB 1 MGVNMM 7

RESULT 10
 ID 09PXC3 PRELIMINARY; PRT; 10 AA.

AC 09PXC3;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE B antigen P20E (Fragment).

OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=92013147; PubMed=1717588;
 RA Takahashi K., Kishimoto S., Ohoi K., Yoshizawa H., Machida A.,
 RA Ohnuma H., Tsuda F., Muneakata E., Miyakawa Y., Mayumi M.;
 RT "Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepatitis B virus";
 RL J. Immunol. 147:3156-3160(1991).
 DR PIR; B46453; B46453.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1238 MW; 485A63AE721E9C7 CRC64;

Query Match 30.5%; Score 18; DB 12; Length 10;
 Best Local Similarity 60.0%; Pred. No. 9.1e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 TOLMHL 9

Db 1 MOLF 5

RESULT 11

Q23876 PRELIMINARY; PRT; 11 AA.
 ID Q23876;
 AC Q23876;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
 DE Actin 4.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
 NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82260445; PubMed=6286214;
 RA McKeeown M., Firtel R.A.;
 RT "Actin multigene family of Dictyostelium";
 RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
 DR EMBL; K02957; AAA3150.1;
 DR EMBL; K02956; AAA3150.1; JOINED.
 SQ SEQUENCE 11 AA; 1205 MW; 728B4C1AC6C2CAAB CRC64;

Query Match 30.5%; Score 18; DB 5; Length 11;
 Best Local Similarity 28.6%; Pred. No. 1e+04; 1; Indels 0; Gaps 0;
 Matches 2; Conservative 4; Mismatches 1;

QY 4 EIQLMNN 10
 Db 5 DVQALNN 11

RESULT 12

Q85631 PRELIMINARY; PRT; 12 AA.
 ID Q85631;
 AC Q85631;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE MH2, proviral DNA, myc to 3' LTR (Fragment).
 OS Avian carcinoma virus.
 OS Viruses; Retrovirdae; Retroviridae; Alpharetrovirus.
 NCBI_TaxID=11958;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85033920; PubMed=6092695;
 RA Sutcliffe P., Jansen H.W., Bister K., Rapp U.R.;
 RT "3'-terminal region of avian carcinoma virus MH2 shares sequence elements with avian sarcoma viruses Y73 and SR-A.";
 RL J. Virol. 52:703-705(1984).
 DR EMBL; K03100; AAA2388.1;
 FT NON_TER 1
 SQ SEQUENCE 12 AA; 1466 MW; 72E4B884F30736DB CRC64;

Query Match 30.5%; Score 18; DB 15; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNL 11
 Db 2 HNL 4

RESULT 13
 Q28742 PRELIMINARY; PRT; 7 AA.
 AC Q28742;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Alpha-myosin heavy chain (Fragment).
 OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84221901; PubMed=6328491;
 RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
 RA Rabinowitz M.;
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-
 ventricular myosin heavy chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
 DR EMBL; K01698; AAA1415.1;
 DR PIR; I46868; I46868.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 916 MW; 6B1B1A1E9326B0 CRC64;

Query Match 28.8%; Score 17; DB 6; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QLMNN 10
 Db 1 QXQHD 5

RESULT 14

Q15891 PRELIMINARY; PRT; 9 AA.
 ID Q15891;
 AC Q15891;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE (Clone XP285B) (Fragment).
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta.
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldwin A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 arrayed cDNAs and cosmid libraries.";
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL; L32131; AAA73861.1;
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1030 MW; E56635A1A3366D1 CRC64;

Query Match 28.8%; Score 17; DB 4; Length 9;
 Best Local Similarity 44.4%; Pred. No. 1e+06;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 EIQLMNLG 12
 Db 1 EHQMKSTSLG 9

RESULT 15

Q96D12 PRELIMINARY; PRT; 9 AA.
 ID Q96D12;
 AC Q96D12;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Ribosomal protein S16 (Fragment).
 GN Rps16.
 OS Lithospadix monostachya.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecoidae;

OC Areceae; Liospadiciinae; Liospadix.
OX NCBI_TaxID=13182;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Aemussen C.B., Chase M.W.;
RT "Coding and noncoding plastid DNA in palm systematics";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ404941; CAC17917.1; -
DR GO; GO:0009507; Chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1106 MW; 1B9236C2C0441B50 CRC64;

Query Match 28.8%; Score 17; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQLM 8
: |||
Db 6 VQLM 9

Search completed: May 18, 2004, 10:04:47
Job time : 32.25 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:42:39 ; Search time 45.75 Seconds
(without alignments)
74.111 Million cell updates/sec

Title: US-09-730-174A-3
Perfect score: 59
Sequence: 1 SEWELQMLHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 50 | 84.7 | 11 | 3 | AA96968 Parathyro |
| 2 | 50 | 84.7 | 11 | 6 | ABG72607 Parathyro |
| 3 | 50 | 84.7 | 12 | 6 | ABG72608 Parathyro |
| 4 | 49 | 83.1 | 10 | 2 | AA91644 Human par |
| 5 | 49 | 83.1 | 10 | 3 | AA91644 Human par |
| 6 | 49 | 83.1 | 10 | 4 | AA91644 Human par |
| 7 | 49 | 83.1 | 10 | 6 | AA91644 Human par |
| 8 | 45 | 76.3 | 9 | 2 | AA91644 Human par |
| 9 | 43 | 72.9 | 9 | 2 | AA91644 Human par |
| 10 | 43 | 72.9 | 9 | 3 | AA91644 Human par |
| 11 | 43 | 72.9 | 9 | 4 | AA91644 Human par |
| 12 | 40.5 | 68.6 | 11 | 2 | AA91644 Human par |
| 13 | 40 | 67.8 | 9 | 3 | AA91644 Human par |
| 14 | 40 | 67.8 | 9 | 3 | AA91644 Human par |
| 15 | 37 | 62.7 | 10 | 3 | AA91644 Human par |
| 16 | 37 | 62.7 | 10 | 4 | AA91644 Human par |
| 17 | 37 | 62.7 | 11 | 4 | AA91644 Human par |
| 18 | 37 | 62.7 | 11 | 4 | AA91644 Human par |
| 19 | 37 | 62.7 | 11 | 4 | AA91644 Human par |
| 20 | 37 | 62.7 | 12 | 4 | AA91644 Human par |
| 21 | 37 | 62.7 | 12 | 4 | AA91644 Human par |
| 22 | 36 | 61.0 | 9 | 3 | AA91644 Human par |
| 23 | 35 | 59.3 | 8 | 3 | AA91644 Human par |
| 24 | 35 | 59.3 | 8 | 3 | AA91644 Human par |
| 25 | 35 | 59.3 | 8 | 4 | AA91644 Human par |

| | | | | | |
|----|----|------|----|---|--------------------|
| 26 | 35 | 59.3 | 10 | 6 | ABP71484 Parathyro |
| 27 | 35 | 59.3 | 11 | 6 | ABP71485 Parathyro |
| 28 | 35 | 59.3 | 11 | 6 | ABP71485 Parathyro |
| 29 | 35 | 59.3 | 12 | 2 | AA91644 Human par |
| 30 | 35 | 59.3 | 12 | 6 | ABP71482 Parathyro |
| 31 | 33 | 55.9 | 9 | 3 | AA91644 Human par |
| 32 | 32 | 54.2 | 11 | 1 | AA91644 Human par |
| 33 | 32 | 54.2 | 11 | 1 | AA91644 Human par |
| 34 | 32 | 54.2 | 12 | 2 | AA91644 Human par |
| 35 | 30 | 50.8 | 7 | 2 | AA91644 Human par |
| 36 | 30 | 50.8 | 7 | 4 | AA91644 Human par |
| 37 | 30 | 50.8 | 9 | 3 | AA91644 Human par |
| 38 | 30 | 50.8 | 9 | 3 | AA91644 Human par |
| 39 | 29 | 49.2 | 10 | 5 | ABG69386 Vascular |
| 40 | 29 | 49.2 | 12 | 5 | AA91644 Human par |
| 41 | 27 | 45.8 | 11 | 4 | ABUS4029 Human DNA |
| 42 | 27 | 45.8 | 12 | 2 | AA91644 Human par |
| 43 | 27 | 45.8 | 12 | 3 | AA91644 Human par |
| 44 | 26 | 44.1 | 6 | 2 | AA91644 Human par |
| 45 | 26 | 44.1 | 6 | 3 | AA91644 Human par |

ALIGNMENTS

RESULT 1
AA96968 standard; peptide; 11 AA.

AA96968 standard; peptide; 11 AA.
AC AA96968;
DT 31-OCT-2000 (first entry)
DE Parathyroid hormone N-terminal signaling domain (residues 1-11).
DE Parathyroid hormone; N-terminal; signaling domain; bone mass;
KM PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW bone reformation; resorption; remodeling; tether1; osteoporosis.
XX Homo sapiens.
XX WO200039278-A2.
XX 06-JUL-2000.
XX 30-DEC-1999; 99WO-US031108.
XX 31-DEC-1998; 98US-0114577P.
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (BOT/) BOTTS J T.
XX (JUEP/) JUEPPNER H.
XX Gardella TV, Kronenberg HM, Fotts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass.
XX Claim 4; Page 92; 119pp; English.
XX Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or S-(L) n
XX -R, are new S is an amino terminal signaling functional domain of
XX parathyroid hormone (PTH), L is a linker molecule present n times (where
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the
XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
XX sequence. The new compounds are used for treating mammalian conditions
XX characterized by decreases in bone mass, determining rates of bone
XX reformation, bone resorption and/or bone remodeling, treating diseases
XX and disorders associated with decreased rethet1 activity, increasing cAMP

CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
 CC non-peptide PTH (claimed). The new compound can be administered by
 CC inhalation unlike the large native PTH or PTHrp which avoids the need for
 CC regular injections to treat osteoporosis

XX Sequence 11 AA;

Query Match 84.7%; Score 50; DB 3; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 1; Indels 0; Gaps 0;
 QY 1 VSEIQMLNML 11
 Db 1 AVSEIQMLNML 11

RESULT 2

ABG72607
 ID ABG72607 standard; peptide; 11 AA.

XX AC ABG72607;

XX DT 11-FEB-2003 (first entry)

XX DE Parathyroid hormone antigenic peptide 2-12.

XX KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
 primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Rattus sp.

XX OS Bos taurus.

XX OS Sus scrofa.

XX OS Canis familiaris.

XX FT Key Location/Qualifiers

XX FT Misc-difference 6 /label= Leu, Phe

XX PN US2002110871-A1.

XX PD 15-AUG-2002.

XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHRA/) ZAHRADNIK R J.

XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX PN WPI; 2003-066685/06.

XX PD 15-AUG-2002.

XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHRA/) ZAHRADNIK R J.

XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX PN WPI; 2003-066685/06.

XX PD 15-AUG-2002.

XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHRA/) ZAHRADNIK R J.

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XX PN WPI; 2003-066685/06.

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XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

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XX PA (LAVI/) LAVIGNE J R.

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XX PN WPI; 2003-066685/06.

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XX PA (LAVI/) LAVIGNE J R.

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XX PN WPI; 2003-066685/06.

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XX PN WPI; 2003-066685/06.

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XX PR 05-DEC-2000; 2000US-00730174.

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XX PA (LAVI/) LAVIGNE J R.

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XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX PN WPI; 2003-066685/06.

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XX PF 05-DEC-2000; 2000US-00730174.

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XX PN WPI; 2003-066685/06.

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XX PN WPI; 2003-066685/06.

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XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

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XX PN WPI; 2003-066685/06.

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XX PF 05-DEC-2000; 2000US-00730174.

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XX PN WPI; 2003-066685/06.

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XX PR 05-DEC-2000; 2000US-00730174.

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XX PN WPI; 2003-066685/06.

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XX PR 05-DEC-2000; 2000US-00730174.

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XX PN WPI; 2003-066685/06.

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XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

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XX PA (LAVI/) LAVIGNE J R.

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XX PN WPI; 2003-066685/06.

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XX PR 05-DEC-2000; 2000US-00730174.

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XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX PN WPI; 2003-066685/06.

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XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHRA/) ZAHRADNIK R J.

XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX PN WPI; 2003-066685/06.

XX PD 15-AUG-2002.

XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHRA/) ZAHRADNIK R J.

XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX PN WPI; 2003-066685/06.

XX PD 15-AUG-2002.

XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHRA/) ZAHRADNIK R J.

XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX PN WPI; 2003-066685/06.

XX PD 15-AUG-2002.

XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHRA/) ZAHRADNIK R J.

XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX PN WPI; 2003-066685/06.

XX PD 15-AUG-2002.

XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHRA/) ZAHRADNIK R J.

XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX PN WPI; 2003-066685/06.

XX PD 15-AUG-2002.

XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHRA/) ZAHRADNIK R J.

XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX PN WPI; 2003-066685/06.

XX PD 15-AUG-2002.

XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHRA/) ZAHRADNIK R J.

XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX PN WPI; 2003-066685/06.

XX PD 15-AUG-2002.

XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-

XX The invention relates to a new antigenic peptide for inducing the
CC formation and isolation of antibodies having an affinity to it, being
CC formed from the N-terminus of parathyroid hormone (PTH). Also included
CC are: (1) a method for producing antibodies useful in the determination of
CC PTH levels in a biological sample comprising: (a) providing at least one
CC first peptide antigen comprising a peptide fragment of PTH; (b)
CC administering the first peptide antigen to a host animal to induce
CC antibody production; (c) monitoring the antibody titre produced; (d)
CC isolating antisera produced in the host animal; and (e) selecting
CC antisera from the isolated antisera produced in the host that is capable
CC of binding to a second peptide antigen; (2) an antibody (ab) produced by
CC the method; and (3) test kits and analytical procedures used for the
CC determination of bioactive intact PTH utilising (ab). The methods and
CC compositions of the present invention are useful for determining
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
CC The antigens, antibodies and methods of the present invention, as
CC compared to prior art, have the particular advantages of possessing
CC greater affinity for PTH, and in particular, are designed to have a novel
CC recognition for amino acid residues extending beyond the first N-terminal
CC PTH residue, and further have negligible cross-reactivity with the large
CC non-molecular forms of PTH. PTH levels are an important parameter in
CC patients suffering from hypercalcaemia, osteoporosis and primary
CC hyperparathyroidism. The present sequence represents a PTH antigenic
CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,
CC canine and bovine PTH
XX

Query Match 84.7%; Score 50; DB 6; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.014; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX

2 VSEIQMLNMG 12
Db 2 VSEIQMLNMG 12

RESULT 4
AAR91644
ID AAR91644 standard; peptide; 10 AA.
XX
AC AAR91644;
XX
DT 06-NOV-1996 (first entry)
XX
DE Human parathyroid hormone antigenic peptide hPTH 1-10.
XX
KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
XX diagnosis; active hPTH 1-37.
XX
OS Synthetic.
XX
PN DE4434551-A1.
XX
PD 04-APR-1996.
XX
PF 26-SEP-1994; 94DE-04434551.
XX
PR 28-SEP-1994; 94DE-04434551.
XX
PA (FORS/) FORSSMANN W.
XX
PI Adermann K, Forssmann W, Hock D, Maegerlein M;
XX
DR WPI; 1996-180391/19.
XX
PT New antigenic peptide(s) from human parathyroid hormone - and antibodies
XX generated using them, able to distinguish between active and inactive
XX forms of the hormone.
XX
PS Claim 2; Page 4; 5pp; German.
XX

CC The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC terminal alpha-helical region and/or the non-structured region of the
CC hormone. Antibodies and their binding fragments generated by injecting an
CC animal with the peptides are useful as diagnostic reagents for
CC determination of biologically active hPTH(1-37)
XX

Sequence 10 AA;
XX

Query Match 83.1%; Score 49; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

1 SVSEIQMLNHN 10
Db 1 SVSEIQMLNHN 10

RESULT 5
AAV68767
ID AAV68767 standard; peptide; 10 AA.
XX
AC AAV68767;
XX
DT 05-MAY-2000 (first entry)
XX
DE Amino acids 1-10 of a parathyroid hormone (PTH).
XX
KW Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;
XX slimming treatment; cellulite; skin firming.
XX
OS Unidentified.
XX
PN WO200004047-A1.
XX
PD 27-JAN-2000.
XX
PF 07-JUL-1999; 99WO-FR001687.
XX
PR 17-JUL-1998; 98FR-00009193.
XX
PA (SEDE-) SEDERMA.
XX
PI Lintner K;
XX
DR WPI; 2000-171243/15.
XX
DE New parathyroid hormone fragment peptides, used as lipolysis stimulants
XX PT in topically applied cosmetic compositions for slimming treatment of
XX PT excessive weight in hips and thighs.
XX
PS Claim 1; Page 6; 18pp; French.
XX
XX The present sequence represents a parathyroid hormone (PTH) fragment,
CC comprising amino acids 1-10. Parathyroid hormone fragments of the
CC invention have lipolytic stimulating activity (especially when topically
CC administered). The lipolytic activity of the peptides is enhanced when
CC they are chemically modified to increase their lipophilicity. The
CC peptides are used in cosmetic or dermatological compositions for skin
CC care. They are especially used for slimming treatment of excessive weight
CC in the thighs and hips, in the treatment of cellulite and for skin
CC firming
XX

Sequence 10 AA;
XX

Query Match 83.1%; Score 49; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

1 SVSEIQMLNHN 10
Db 1 SVSEIQMLNHN 10

RESULT 6
 AAB86219
 ID AAB86219 standard; peptide; 10 AA.
 AC AAB86219;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human parathyroid hormone immunogenic peptide SEQ ID 1.
 DE Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
 KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
 KW hypo-parathyroidism; hyper-parathyroidism.
 XX
 OS Homo sapiens.
 XX
 FN DE19961350-A1.
 PD 21-JUN-2001.
 XX
 PF 17-DEC-1999; 99DE-01061350.
 XX
 PR 17-DEC-1999; 99DE-01061350.
 XX
 PA (IMMU-) IMMUNODIAGNOSTIK AG.
 XX
 PI Ambaxter FP;
 XX
 DR WPI; 2001-376318/40.
 XX
 PT Determining the content of physiologically active parathyroid hormone,
 PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
 PT reactive with different epitopes.
 XX
 PS Disclosure; Page 3; 10pp; German.
 XX
 CC This invention describes a novel method for determining (M1) the content
 CC of active parathyroid hormone (A) by treating a sample with (i) antibody
 CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
 CC and including the N-terminal residue and (ii) antibody (Ab2) that
 CC recognizes an epitope within the receptor-binding site of (A). The number
 CC of molecules that react with both antibodies is determined and used to
 CC calculate the content of physiologically active (A). The method is used
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that
 CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
 CC active and (ii) that apparently intact peptide may be biologically
 CC inactive, and also takes into account the fact that some fragments of (A)
 CC are antagonistic (these have the receptor-binding site but lack the N-
 CC terminus). It thus provides a true measure of the content of
 CC physiologically active (A), contrast methods that measure intact peptide
 CC and its 1-37 fragment which may produce falsely high values. This
 CC sequence represents a peptide fragment used to illustrate the method of
 CC the invention
 XX
 SQ Sequence 10 AA;

Query March 83.1%; Score 49; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMHN 10
 DB 1 SVSEIQLMHN 10
 XX
 RESULT 7
 ABR44166
 ID ABR44166 standard; peptide; 10 AA.
 XX
 AC ABR44166;
 XX

DT 04-AUG-2003 (first entry)
 XX
 DE Human parathyroid hormone (hPTH) fragment (residues 1-10).
 XX
 KW Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;
 KW lipolysis; human; hPTH.
 XX
 OS Homo sapiens.
 XX
 FN WO2003035697-A1.
 PD 01-MAY-2003.
 XX
 PF 06-MAY-2002; 2002WO-KR000835.
 XX
 PR 27-SEP-2001; 2001KR-00060245.
 PR 15-MAR-2002; 2002KR-00014062.
 XX
 PA (GLDS) LG HOUSEHOLD & HEALTH CARE LTD.
 XX
 PI Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H,
 PI Chang M;
 XX
 DR WPI; 2003-468288/44.
 XX
 PT Novel fusion peptide comprising self cell-penetrating Tat peptide bound
 PT to human parathyroid hormone-derived peptide, useful as component of skin
 PT slimming cosmetic composition.
 XX
 PS Claim 5; Page 6; 32pp; English.
 XX
 CC The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-
 CC penetrating Tat peptide is bound to human parathyroid hormone-derived
 CC peptide (hPTHDP). The fusion peptide is useful as a component of skin
 CC slimming cosmetic composition. The fusion peptide does not cause
 CC irritation, easily and safely penetrates into integument and endothelium,
 CC does not cause skin disease and has superior lipolysis effects, and is
 CC durable. The present sequence represents a human parathyroid hormone
 CC (hPTH) fragment that can be used to construct the fusion peptide
 XX
 SQ Sequence 10 AA;

Query March 83.1%; Score 49; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEIQLMHN 10
 DB 1 SVSEIQLMHN 10
 XX

RESULT 8
 AAB86225
 ID AAB86225 standard; peptide; 9 AA.
 AC AAB86225;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human parathyroid hormone immunogenic peptide SEQ ID 7.
 DE Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
 KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
 KW hypo-parathyroidism; hyper-parathyroidism.
 XX
 OS Homo sapiens.
 XX
 FN DE19961350-A1.
 PD 21-JUN-2001.
 XX
 PF 17-DEC-1999; 99DE-01061350.
 XX

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XX 17-DEC-1999;      99DE-01061350.
XX PA              (IMMU-) IMMUNDIAGNOSTIK AG.
XX PI              Armbruster FP;
XX DR              WPI ; 2001-376318/40.
XX PT              Determining the content of physiologically active parathyroid hormone,
XX PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
XX PT reactive with different epitopes.
PS Disclosure; Page 3, 10pp; German.
XX
CC This invention describes a novel method for determining (M1) the content
CC of active parathyroid hormone (A) by treating a sample with (i) antibody
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (ii) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyperparathyroidism. The method (unlike known assays) recognizes that
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (ii) that apparently interact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention
XX
SO Sequence 9 AA:
XX
Query Match          76.3%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      2 VSEIQLMHN 10
        |||||
Db       1 VSEIQLMHN 9
RESULT 9
AAR91645 AAR91645 standard; peptide; 9 AA.
AC AAR91645;
DT 06-NOV-1996 (first entry)
DE Human parathyroid hormone antigenic peptide hPTH 1-9.
KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
KW diagnosis; active hPTH 1-37.
OS Synthetic.
XX DE4434551-A1.
XX EN
XX PD 04-APR-1996.
XX PF 28-SEP-1994; 94DE-04434551.
XX PR 28-SEP-1994; 94DE-04434551.
XX (FORS/) FORSSMANN W.
XX Adermann K., Forssmann W., Hock D., Maegerlein M;
XX WPI , 1996-180391/19.

```

PT New antigenic peptide(s) from human parathyroid hormone - and antibodies
PT generated using them, able to distinguish between active and inactive
PS forms of the hormone.

XX
PS Claim 2; Page 4; 5pp; German.

CC The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC terminal alpha-helical region and/or the non-structured region of the
CC hormone. Antibodies and their binding fragments generated by injecting an
CC animal with the peptides are useful as diagnostic reagents for
CC determination of biologically active hPTH(1-37)

XX
SQ Sequence 9 AA;

Query Match 72.9%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 SVSEIQLMH 9
|||
Dd 1 SVSEIQLMH 9

RESULT 10
AAy96981
ID AAy96981 standard; peptide; 9 AA.
AC AAY96981;
XX
XX AAY96981;
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain.
XX
KM PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW bone reformation; resorption; remodeling; tether; osteoporosis.
XX
OS Homo sapiens.
XX
PV WO200039278-A2.
XX
BD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-C114577P.
XX
PA (GARD/) GARDELIA T J.
PA (KRON/) KROENENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
Xx Gardella TJ, Kronenberg HM, Potts JT, Jueppner H,
Pl
DR WPI: 2000-452384/39.
XX
XX New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
XX Claim 11; Page 93; 119pp; English.

CC Compounds of the structure or formula S-(L)_n-B, R₁S-(L)_n-R or S-(L)_n-
CC-R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R₁ is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased bone activity, increasing BMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or

CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis

SO Sequence 9 AA;

Query Match 72.9%; Score 43; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9
DB 1 SVSEIQLMH 9

RESULT 11
ID AAB86220 standard; peptide: 9 AA.

XX AAB86220;
AC AAB86220;
XX 03-SEP-2001 (first entry)

XX Human parathyroid hormone immunogenic peptide SEQ ID 2.

XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW hypo-parathyroidism; hyper-parathyroidism.

XX Homo sapiens.

XX DE19961350-A1.

XX 21-JUN-2001.

XX 17-DEC-1999; 99DE-01061350.

XX 17-DEC-1999; 99DE-01061350.

XX (IMMU-) IMMUNDIAGNOSTIK AG.

XX Armbruster FP;

XX WPI; 2001-376318/40.

XX Determining the content of physiologically active parathyroid hormone,
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT reactive with different epitopes.

XX Disclosure; Page 3; 10pp; German.

XX This invention describes a novel method for determining (M) the content
CC of active parathyroid hormone (A) by treating a sample with (i) antibody
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (ii) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyper-parathyroidism. The method (unlike known assays) recognizes that
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (ii) that apparently intact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention

XX Sequence 9 AA;

Query Match 72.9%; Score 43; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9
DB 1 SVSEIQLMH 9

RESULT 12
ID AAY50600 standard; peptide: 11 AA.

XX AAY50600;
AC AAY50600;
XX 09-FEB-2000 (first entry)

XX Resin bound cyclic peptide 33.

XX Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;
KW hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;
KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;
KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "FMOC-Ala"

FT Misc-difference 3 /note= "Ser(OrBu)"

FT Misc-difference 4 /note= "Glu(OrBu)"

FT Misc-difference 6 /note= "Gln(Trt)"

FT Misc-difference 9 /note= "His(Trt)"

FT Misc-difference 10 /note= "Asn(Trt)"

XX WO9552933-A1.

XX 21-OCT-1999.

XX 15-APR-1999; 99WO-US008435.

XX 15-APR-1998; 98US-0081897P.

XX (RHON) RHONE-POULENC RORER PHARM INC.

XX Sledeski AW, Mancel JU;

XX WPI; 1999-633822/54.

XX Convergent synthesis of peptides for treating e.g. bone disorders.

XX Disclosure; Page 75; 85pp; English.

XX This invention describes a novel method for the preparation of peptides
CC (ii) that contain both cyclic and linear peptide fragments comprises
CC sequential reaction of a resin-bound linear fragment with the cyclic
CC fragment in N-protected form and optionally other linear fragments. The
CC products of the invention have osteopathic and hypotensive activity (ii)
CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The
CC method is particularly used to prepare cyclic peptide analogs of
CC parathyroid hormone (PTH) or PTH-related peptides which are useful for
CC treating diseases that respond to treatment with agents that bind to PTH
CC receptors (with or without activation of adenyl cyclase activity), e.g.
CC hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-
CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also
CC for promoting repair of bone fractures. Separate synthesis of the cyclic
CC fragment allows convergent synthesis of resin-bound (ii), with better
CC yields and higher throughput. The difficulties associated with
CC preparation of the bridged fragment are confined to a small peptide which

CC can be purified before reaction with the resin-bound component. AAY50568-
CC Y50614 represent the peptide fragments described in the method of the
CC invention
XX
SQ Sequence 11 AA;
Query Match 68.6%; Score 40.5; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 0.73;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 SVSEIOLMNLG 12
:|||||
DB 1 AVSEIOL-NHLG 11
RESULT 13
AAB01862
ID AAB01862 standard; peptide, 9 AA.
XX
XX AAB01862;
XX
DT 11-SEP-2000 (first entry)
XX PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.
XX
XX Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KM calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
KM bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200023594-A1.
XX
XX 27-APR-2000.
XX
XX 20-OCT-1999; 99WO-US024481.
XX
XX 22-OCT-1998; 98US-0105530P.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX Gardeila TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-339693/29.
XX
XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
XX acids that encode them, useful for treating osteoporosis.
XX
XX Disclosure; Page 26; 73pp; English.
XX
XX The invention relates to a novel parathyroid hormone (PTH) peptide
XX (AAB01859) and parathyroid hormone-related peptide (PTHrP, AAB01860), and
XX biologically active derivatives thereof (AAB01857-B01858, AAB01861-
XX B01869). The peptides of the invention are at least 85% identical to the
XX generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
XX Gly-Tyr-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Tyr; X3 is
XX Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Tyr; X6 is His or Ser;
XX provided that the peptide is not PTHrP(1-14). The peptides of the
XX invention also encompass fragments of peptides of the invention
XX consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
XX terminal derivatives. PTH is a major regulator of calcium homeostasis,
XX and is necessary for the normal function of the gastrointestinal,
XX skeletal, neurological system, neuromuscular and cardiovascular systems.
XX It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
XX and to the recently identified PTH-2 receptor. PTH has a potent anabolic
XX effect on the skeleton, and mediates calcium reabsorption, enhances
XX phosphate clearance and vitamin D synthesis in the kidney. A homologous
XX calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
XX the renal and skeletal actions of PTH, and also bind to the PTH-1

CC receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01859,
CC AAB01861-B01869) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC conditions characterized by a decrease in bone mass, such as
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC medical disorders that arise from excessive or altered action of the PTH-
CC 1/PTH-2 receptor. Detectably labeled peptides of the invention are also
CC useful in the determination of rates of bone formation, bone resorption
CC and/or bone remodeling in a patient. The peptides of the invention are
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC conventional synthetic chemistry, and can be delivered to a patient via
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC PTH-1/PTH-2 receptor agonists
XX
SQ Sequence 9 AA;
Query Match 67.8%; Score 40; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVSEIOLMNLG 9
:|||||
DB 1 AVSEIOLMNLG 9
RESULT 14
AAY6966
ID AAY6966 standard; peptide, 9 AA.
XX
XX AAY6966;
XX
XX 31-OCT-2000 (first entry)
XX
XX Parathyroid hormone N-terminal signaling domain (residues 1-9).
XX
XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KM bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
XX Homo sapiens.
XX
XX WO200039278-A2.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US031108.
XX
XX 31-DEC-1998; 98US-0114577P.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX Gardeila TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452364/39.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass.
XX
XX Claim 4; Page 92; 119pp; English.
XX
XX Compounds of the structure or formula S-(L) n-B, R 1-8-(L) n-R or S-(L) n
XX -R, are new. S is an amino terminal signaling functional domain of
XX parathyroid hormone (PTH); L is a linker molecule present n times (where
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the
XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
XX sequence. The new compounds are used for treating mammalian conditions
XX characterized by decreases in bone mass, determining rates of bone
XX reformation, bone resorption and/or bone remodeling, treating diseases

CC and disorders associated with decreased tether1 activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 9 AA:
Query Match 67.8%; Score 40; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVSEIQLMH 9
Db 1 AVSEIQLMH 9
RESULT 15
AAB01863
ID AAB01863 standard; peptide; 9 AA.
XX
AC AAB01863;
XX
DT 11-SEP-2000 (first entry)
XX
DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.
XX
KM Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KM calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
KM bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200023594-A1.
XX
PD 27-APR-2000.
XX
PF 20-OCT-1999; 99WO-US024481.
XX
PR 22-OCT-1998; 98US-0105530P.
XX
PA (GARD/) GARDILA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPNER H.
XX
PI Gardeila TJ, Kronenberg HM, Potts JT, Tueppner H;
XX
DE WPI: 2000-339693/29.
XX
PT Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
PT acids that encode them, useful for treating osteoporosis.
XX
PS Disclosure: Page 26; 73pp; English.
XX
CC The invention relates to a novel parathyroid hormone (PTH) peptide
CC (AAB01859) and parathyroid hormone-related peptide (PTHrP, AAB01860), and
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC B01869). The peptides of the invention are at least 85% identical to the
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC provided that the peptide is not PTHrP(1-14). The peptides of the
CC invention also encompass fragments of peptides of the invention
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC and is necessary for the normal function of the gastrointestinal,
CC skeletal, neurological system, neuromuscular and cardiovascular systems.
CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC effect on the skeleton, and mediates calcium reabsorption, enhances
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous

CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC the renal and skeletal actions of PTH, and also bind to the PTH-1
CC receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC conditions characterized by a decrease in bone mass, such as
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC medical disorders that arise from excessive or altered action of the PTH-
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC useful in the determination of rates of bone formation, bone resorption
CC and/or bone remodeling in a patient. The peptides of the invention are
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC conventional synthetic chemistry, and can be delivered to a patient via
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC PTH-1/PTH-2 receptor agonists
XX
SQ Sequence 9 AA:
Query Match 62.7%; Score 37; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVSEIQLMH 9
Db 1 AVSEIQLMH 9

Search completed: May 18, 2004, 10:01:53
Job time : 46.75 secs

Tue May 18 12:03:00 2004

us-09-730-174a-3.closed.rapb

Page 1

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OM protein - protein search, using sw model

Run on: May 18, 2004, 10:04:51 ; Search time 33.25 Seconds
(without alignments)
100.425 Million cell updates/sec

Title: US-09-730-174A-3
Perfect score: 59
Sequence: 1 SVSEIQMHNIG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145566 segs, 278261457 residues

Total number of hits satisfying chosen parameters: 166097

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 59 | 100.0 | 12 | 9 | US-09-730-174A-3 |
| 2 | 56 | 94.9 | 12 | 9 | US-09-730-174A-5 |
| 3 | 55 | 93.2 | 11 | 9 | US-09-730-174A-1 |
| 4 | 55 | 93.2 | 12 | 9 | US-09-730-174A-4 |
| 5 | 52 | 88.1 | 12 | 9 | US-09-730-174A-6 |
| 6 | 51 | 86.4 | 11 | 9 | US-09-730-174A-2 |
| 7 | 49 | 83.1 | 10 | 14 | US-10-168-185-1 |
| 8 | 45 | 76.3 | 9 | 14 | US-10-168-185-7 |
| 9 | 43 | 72.9 | 9 | 14 | US-10-168-185-2 |
| 10 | 41 | 69.5 | 8 | 14 | US-10-168-185-8 |
| 11 | 40 | 67.8 | 9 | 14 | US-10-192-673-6 |
| 12 | 37 | 62.7 | 9 | 14 | US-10-192-673-7 |
| 13 | 35 | 59.3 | 8 | 14 | US-10-168-185-3 |
| 14 | 33 | 55.9 | 9 | 14 | US-10-192-673-10 |
| 15 | 30 | 50.8 | 7 | 14 | US-10-168-185-4 |

| | | | | | | |
|----|----|------|----|----|-------------------|--------------------|
| 16 | 30 | 50.8 | 9 | 14 | US-10-192-673-8 | Sequence 8, Appli |
| 17 | 29 | 49.2 | 10 | 14 | US-10-033-741-61 | Sequence 61, Appl |
| 18 | 28 | 47.5 | 9 | 9 | US-09-746-945-6 | Sequence 6, Appli |
| 19 | 28 | 47.5 | 12 | 14 | US-10-319-130-16 | Sequence 16, Appli |
| 20 | 26 | 44.1 | 6 | 14 | US-10-168-185-5 | Sequence 5, Appli |
| 21 | 26 | 44.1 | 10 | 14 | US-10-168-185-11 | Sequence 11, Appli |
| 22 | 25 | 42.4 | 11 | 12 | US-09-747-287-185 | Sequence 185, App |
| 23 | 24 | 40.7 | 10 | 9 | US-09-826-290-27 | Sequence 27, Appli |
| 24 | 24 | 40.7 | 10 | 16 | US-10-264-309-369 | Sequence 369, App |
| 25 | 24 | 40.7 | 11 | 12 | US-10-609-217-41 | Sequence 41, Appli |
| 26 | 24 | 40.7 | 11 | 12 | US-10-632-388-41 | Sequence 41, Appli |
| 27 | 24 | 40.7 | 11 | 12 | US-10-651-723-41 | Sequence 41, Appli |
| 28 | 24 | 40.7 | 11 | 12 | US-10-645-761-41 | Sequence 41, Appli |
| 29 | 24 | 40.7 | 11 | 16 | US-10-666-696-41 | Sequence 41, Appli |
| 30 | 24 | 40.7 | 11 | 16 | US-10-653-048-41 | Sequence 41, Appli |
| 31 | 24 | 40.7 | 12 | 14 | US-10-286-457-284 | Sequence 284, App |
| 32 | 23 | 39.0 | 7 | 14 | US-10-286-457-469 | Sequence 469, App |
| 33 | 23 | 39.0 | 7 | 15 | US-10-368-280-12 | Sequence 12, Appli |
| 34 | 23 | 39.0 | 7 | 15 | US-10-374-035-12 | Sequence 12, Appli |
| 35 | 23 | 39.0 | 9 | 9 | US-09-894-018-332 | Sequence 332, App |
| 36 | 23 | 39.0 | 9 | 10 | US-09-821-734-4 | Sequence 4, Appli |
| 37 | 23 | 39.0 | 9 | 10 | US-09-854-248-11 | Sequence 285, App |
| 38 | 23 | 39.0 | 9 | 12 | US-10-953-286-288 | Sequence 50, Appli |
| 39 | 23 | 39.0 | 9 | 14 | US-10-094-699-50 | Sequence 288, App |
| 40 | 23 | 39.0 | 9 | 15 | US-10-117-937-249 | Sequence 249, App |
| 41 | 23 | 39.0 | 9 | 15 | US-10-245-871-288 | Sequence 288, App |
| 42 | 23 | 39.0 | 10 | 14 | US-10-094-699-49 | Sequence 49, Appli |
| 43 | 23 | 39.0 | 10 | 15 | US-10-026-066-31 | Sequence 31, Appli |
| 44 | 23 | 39.0 | 10 | 15 | US-10-026-066-83 | Sequence 83, Appli |
| 45 | 23 | 39.0 | 10 | 15 | US-10-117-937-248 | Sequence 248, App |

ALIGNMENTS

RESULT 1
US-09-730-174A-3
Sequence 3, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
FILE REFERENCE: IMUNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 3
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3

Query Match 100.0%; Score 59; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SVSEIQMHNIG 12
Db 1 SVSEIQMHNIG 12

RESULT 2
US-09-730-174A-5
Sequence 5, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
FILE REFERENCE: IMUNE-001A

CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 5
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5

Query Match 94.9%; Score 56; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0024;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQMHNIG 12
Db 1 AVSEIQMHNIG 12

RESULT 3
US-09-730-174A-1
Sequence 1, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
FILE REFERENCE: IMNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 1
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1

Query Match 93.2%; Score 55; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQMHNIG 12
Db 1 VSEIQMHNIG 11

RESULT 4
US-09-730-174A-4
Sequence 4, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
FILE REFERENCE: IMNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 4
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4

Query Match 93.2%; Score 55; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQMHNIG 12
Db 1 SVSEIQMHNIG 12

RESULT 5
US-09-730-174A-6
Sequence 6, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
FILE REFERENCE: IMNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 6
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-6

Query Match 88.1%; Score 52; DB 9; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.012;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQMHNIG 12
Db 1 AVSEIQMHNIG 12

RESULT 6
US-09-730-174A-2
Sequence 2, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
FILE REFERENCE: IMNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-2

Query Match 86.4%; Score 51; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQMHNIG 12
Db 1 VSEIQMHNIG 11

RESULT 7
US-10-166-185-1
Sequence 1, Application US/10166185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Misbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jürgen
TITLE OF INVENTION: Method for Determining Parathormone

```

; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-1

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```

Query Match      83.1%; Score 49; DB 14; Length 10;
Best Local Similarity 100.0%; Pred.No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 SVSEIQLMHN 10
Db 1 SVSEIQLMHN 10

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```

RESULT 8
US-10-168-185-7
; Sequence 7, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Misbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-7

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Query Match      76.3%; Score 45; DB 14; Length 9;
Best Local Similarity 100.0%; Pred.No. 1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 VSEIQLMHN 10
Db 1 VSEIQLMHN 9

```

```

RESULT 9
US-10-168-185-2
; Sequence 2, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Misbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185

```

```

; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-2

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```

Query Match      72.9%; Score 43; DB 14; Length 9;
Best Local Similarity 100.0%; Pred.No. 1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy 1 SVSEIQLMH 9
Db 1 SVSEIQLMH 9

```

```

RESULT 10
US-10-168-185-8
; Sequence 8, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Misbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-8

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```

Query Match      69.5%; Score 41; DB 14; Length 8;
Best Local Similarity 100.0%; Pred.No. 1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```
Qy 3 SEIQLMHN 10
Db 1 SEIQLMHN 8

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RESULT 11
US-10-192-673-6
; Sequence 6, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379

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PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-192-673-6

Query Match 67.8%; Score 40; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9
Db 1 AVSEIQLMH 9

RESULT 12
US-10-192-673-7
Sequence 7, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
FILE REFERENCE: 0609, 4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-192-673-7

Query Match 62.7%; Score 37; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9
Db 1 AVSEIQLMH 9

RESULT 13
US-10-168-185-3
Sequence 3, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jürgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample

FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-185-3

Query Match 59.3%; Score 35; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 8
Db 1 SVSEIQLMH 8

RESULT 14
US-10-192-673-10
Sequence 10, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
FILE REFERENCE: 0609, 4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-192-673-10

Query Match 55.9%; Score 33; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9
Db 1 SVSEIQLMH 9

RESULT 15
US-10-168-185-4
Sequence 4, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jürgen
TITLE OF INVENTION: Method for Determining Parathormone

; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-4

Query Match 50.8%; Score 30; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIOL 7
Db 1 SVSEIOL 7

Search completed: May 18, 2004, 10:20:59
Job time : 33.25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:58:45 ; Search time 12.75 Seconds
(without alignments)
48.589 Million cell updates/sec

Title: US-09-730-174A-3
Perfect score: 59
Sequence: 1 SVSEIQLMHNIG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 50 | 84.7 | 12 | 4 | US-09-442-989-31 |
| 2 | 49 | 83.1 | 10 | 3 | US-08-817-547A-1 |
| 3 | 43 | 72.9 | 9 | 3 | US-08-817-547A-2 |
| 4 | 40 | 67.8 | 9 | 4 | US-09-421-379-6 |
| 5 | 37 | 62.7 | 9 | 4 | US-09-421-379-7 |
| 6 | 35 | 59.3 | 8 | 3 | US-08-817-547A-3 |
| 7 | 33 | 55.9 | 9 | 4 | US-09-421-379-10 |
| 8 | 32 | 54.2 | 11 | 6 | 5460978-3 |
| 9 | 30 | 50.8 | 7 | 3 | US-08-817-547A-4 |
| 10 | 30 | 50.8 | 9 | 4 | US-09-421-379-8 |
| 11 | 26 | 44.1 | 6 | 3 | US-08-817-547A-5 |
| 12 | 26 | 44.1 | 10 | 2 | US-08-428-257A-14 |
| 13 | 25 | 42.4 | 11 | 3 | US-08-802-981-124 |
| 14 | 24 | 40.7 | 5 | 2 | US-08-177-109A-56 |
| 15 | 24 | 40.7 | 5 | 2 | US-08-687-706-56 |
| 16 | 24 | 40.7 | 5 | 3 | US-08-817-547A-17 |
| 17 | 24 | 40.7 | 6 | 3 | US-08-817-547A-16 |
| 18 | 24 | 40.7 | 7 | 3 | US-08-817-547A-15 |
| 19 | 24 | 40.7 | 8 | 3 | US-08-748-021-64 |
| 20 | 24 | 40.7 | 8 | 3 | US-08-817-547A-14 |
| 21 | 24 | 40.7 | 8 | 3 | US-08-874-297-64 |
| 22 | 24 | 40.7 | 9 | 3 | US-08-817-547A-13 |
| 23 | 24 | 40.7 | 10 | 3 | US-08-817-547A-7 |
| 24 | 24 | 40.7 | 11 | 3 | US-08-726-464B-13 |
| 25 | 24 | 40.7 | 11 | 4 | US-09-428-082B-41 |
| 26 | 23 | 39.0 | 7 | 4 | US-09-336-093-12 |
| 27 | 23 | 39.0 | 7 | 4 | US-09-557-465D-12 |

| | | | | | | |
|----|----|------|----|---|--------------------|--------------------|
| 28 | 23 | 39.0 | 10 | 3 | US-08-396-285-6 | Sequence 6, Appl |
| 29 | 23 | 39.0 | 10 | 4 | US-09-287-221-6 | Sequence 6, Appl |
| 30 | 23 | 39.0 | 12 | 2 | US-08-140-137A-42 | Sequence 42, Appl |
| 31 | 23 | 39.0 | 12 | 4 | US-08-474-349A-271 | Sequence 271, Appl |
| 32 | 22 | 37.3 | 8 | 3 | US-08-160-604-74 | Sequence 74, Appl |
| 33 | 22 | 37.3 | 8 | 3 | US-08-160-604-75 | Sequence 75, Appl |
| 34 | 22 | 37.3 | 8 | 4 | US-09-296-089-10 | Sequence 10, Appl |
| 35 | 22 | 37.3 | 8 | 4 | US-09-551-976-10 | Sequence 10, Appl |
| 36 | 22 | 37.3 | 9 | 4 | US-09-482-543-177 | Sequence 177, Appl |
| 37 | 22 | 37.3 | 10 | 2 | US-08-248-839C-180 | Sequence 180, App |
| 38 | 22 | 37.3 | 11 | 3 | US-08-160-604-73 | Sequence 73, Appl |
| 39 | 22 | 37.3 | 11 | 4 | US-09-296-089-27 | Sequence 27, Appl |
| 40 | 22 | 37.3 | 11 | 4 | US-08-475-955-56 | Sequence 56, Appl |
| 41 | 22 | 37.3 | 11 | 4 | US-09-551-976-27 | Sequence 27, Appl |
| 42 | 22 | 37.3 | 12 | 4 | US-09-690-454-89 | Sequence 89, Appl |
| 43 | 22 | 37.3 | 12 | 4 | US-09-591-694-41 | Sequence 41, Appl |
| 44 | 21 | 35.6 | 5 | 3 | US-08-817-547A-6 | Sequence 6, Appl |
| 45 | 21 | 35.6 | 6 | 2 | US-08-621-803-184 | Sequence 184, App |

ALIGNMENTS

RESULT 1
US-09-442-989-31
; Sequence 31, Application US/09442989
; Patent No. 6569993
; GENERAL INFORMATION:
; APPLICANT: Sledeski, Adam W.
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
; FILE REFERENCE: A311B-US
; CURRENT APPLICATION NUMBER: US/09/442,989
; EARLIER FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: 60/081,897
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentm Ver. 2.1
; SEQ ID NO 31
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)
; OTHER INFORMATION: FMOC-Ala
; NAME/KEY: PEPTIDE
; LOCATION: (3)
; OTHER INFORMATION: Ser(OcBu)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (4)
; OTHER INFORMATION: Glu(OcBu)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (6)
; OTHER INFORMATION: Glu(Trc)
; NAME/KEY: PEPTIDE
; LOCATION: (9)
; OTHER INFORMATION: His(Trc)
; NAME/KEY: PEPTIDE
; LOCATION: (10)
; OTHER INFORMATION: Asn(Trc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: Nle
; US-09-442-989-31

Tue May 18 12:02:59 2004

us-09-730-174a-3.closed.ra1

Page 2

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Query Match      84.7% Score 50; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.0045;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 SVSEIQLMHNIG 12
       :|||||
Db      1 AVSEIQLMHNIG 12

RESULT 2
US-08-817-547A-1
; Sequence 1, Application US/08817547A
; Patent No. 6030790
; GENERAL INFORMATION:
; APPLICANT: Adernann, Knut
; APPLICANT: Hock, Dieter
; APPLICANT: Magerlein, Markus
; TITLE OF INVENTION: Peptides from the hPTH Sequence
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,547A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03757
; FILING DATE: 29 SEPT 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FROST, ROGER T.
; REGISTRATION NUMBER: 22,176
; REFERENCE/DOCKET NUMBER: 07826-0007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: no
; ANTI-SENSE: no
US-08-817-547A-1

Query Match      83.1% Score 49; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVSEIQLMHN 10
       :|||||
Db      1 SVSEIQLMHN 10

RESULT 3
US-08-817-547A-2
; Sequence 2, Application US/08817547A
; Patent No. 6030790
; GENERAL INFORMATION:
; APPLICANT: Adernann, Knut
; APPLICANT: Hock, Dieter
; APPLICANT: Magerlein, Markus
; TITLE OF INVENTION: Peptides from the hPTH Sequence
```

```
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,547A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03757
; FILING DATE: 29 SEPT 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FROST, ROGER T.
; REGISTRATION NUMBER: 22,176
; REFERENCE/DOCKET NUMBER: 07826-0007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: no
; ANTI-SENSE: no
US-08-817-547A-2

Query Match      72.9% Score 43; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVSEIQLMH 9
       :|||||
Db      1 SVSEIQLMH 9

RESULT 4
US-09-421-379-6
; Sequence 6, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
; APPLICANT: Gardella, Henry J.
; APPLICANT: Kronenberg, Thomas J.
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; FILE REFERENCE: 0609,4570001
; CURRENT APPLICATION NUMBER: US/09/421,379
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: U.S. 60/105,530
; EARLIER FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: Peptide
US-09-421-379-6
```

Query Match 67.8%; Score 40; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9
DB 1 AVSEIQLMH 9

RESULT 5
US-09-421-379-7
Sequence 7, Application US/09421379
Patent No. 6495662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
FILE REFERENCE: 0609.4570001
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-7

Query Match 62.7%; Score 37; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9
DB 1 AVSEIQLMH 9

RESULT 6
US-08-817-547A-3
Sequence 3, Application US/08817547A
Patent No. 6030790
GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magelrein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/08/817,547A
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-817-547A-3

Query Match 59.3%; Score 35; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLM 8
DB 1 SVSEIQLM 8

RESULT 7
US-09-421-379-10
Sequence 10, Application US/09421379
Patent No. 6495662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
FILE REFERENCE: 0609.4570001
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-10

Query Match 55.9%; Score 33; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9
DB 1 SVSEIQLMH 9

RESULT 8
5460978-3
Patent No. 5460978
APPLICANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,
BRUCE E.; WETENHALL, RICHARD E.H.
TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL
HYPERCALCEMIA OF MALIGNANCY-BTHRP

NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/715,280
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 199,235
FILING DATE: 09-MAY-1988
APPLICATION NUMBER:
FILING DATE:
SEQ ID NO.3:
LENGTH: 11
5460978-3

Query Match 54.2%; Score 32; DB 6; Length 11;
Best Local Similarity 70.0%; Pred. No. 8.2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 1 SVSEIQLMHN 10
Db 1 AVSEHQLEHN 10

RESULT 9
US-08-817-547A-4
Sequence 4, Application US/08817547A
Patent No. 6030790

GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A

FILING DATE:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994

ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.

REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007

TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700

TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids

TYPE: amino acid
STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: peptide

HYPOTHETICAL: no
ANTI-SENSE: no

US-08-817-547A-4

Query Match 50.8%; Score 30; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SVSEIQL 7

Db 1 SVSEIQL 7

RESULT 10
US-09-421-379-8
Sequence 8, Application US/09421379
Patent No. 6495662

GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potes, John T.

APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid

TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)
FILE REFERENCE: 0609,4570001

CURRENT APPLICATION NUMBER: US/09/421,379
CURRENT FILING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22

NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8
LENGTH: 9

TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-421-379-8

Query Match 50.8%; Score 30; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 SVSEIQLMHN 9
Db 1 AVSEHQLEHN 9

RESULT 11
US-08-817-547A-5

Sequence 5, Application US/08817547A
Patent No. 6030790

GENERAL INFORMATION:
APPLICANT: Adermann, Knut

APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus

TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP

STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta

STATE: Georgia
COUNTRY: USA

ZIP: 30303
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A

FILING DATE:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994

ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.

REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007

US-08-817-547A-4

Query Match 50.8%; Score 30; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SVSEIQL 7

TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-817-547A-5

Query Match 44.1%; Score 26; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQ 6
Db 1 SVSEIQ 6

RESULT 12
US-08-428-257A-14
Sequence 14, Application US/08428257A
Patent No. 5865808
GENERAL INFORMATION:
APPLICANT: Spooner, Robert A.
APPLICANT: Epenetos, A. A.
TITLE OF INVENTION: Compounds to target cells
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,257A
FILING DATE: 07/05/95
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-257A-14

Query Match 44.1%; Score 26; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 94; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIOL 7
Db 3 TVSEVOL 9

RESULT 13
US-08-802-981-124
Sequence 124, Application US/08802981
Patent No. 6037137
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme

TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /product= "Aib"
US-08-802-981-124

Query Match 42.4%; Score 25; DB 3; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 QLMHN 10
Db 5 QLMHN 9

RESULT 14
US-08-177-109A-56
Sequence 56, Application US/08177109A
Patent No. 5865615
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/177,109A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

Tue May 18 12:02:59 2004

us-09-730-174a-3.closed.ra1

Page 6

NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-177-109A-56

Query Match 40.7%; Score 24; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 8 MNLG 12
:|:|
Db 1 LNMWG 5

RESULT 15
US-08-687-706-56
Sequence 56, Application US/08687706
Patent No. 5828892
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESS: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,706
FILING DATE: 26-JUL-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,109
FILING DATE: 03-JAN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 107 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-687-706-56

Query Match 40.7%; Score 24; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 8 MNLG 12
:|:|
Db 1 LNMWG 5

Search completed: May 18, 2004, 10:06:43
Job time : 12.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:56:10 ; Search time 10.25 Seconds
(without alignments)

112.614 Million cell updates/sec

Title: US-09-730-174a-4
Perfect score: 61
Sequence: 1 SVSEIQFMNMG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.78:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|--------|-----------------------|
| 1 | 23 | 37.7 | 10 | 2 | S28055 | cytochrome b559 co |
| 2 | 18 | 29.5 | 7 | 2 | A58718 | carotenoid U149 - Ca |
| 3 | 18 | 29.5 | 9 | 2 | S78420 | ribosomal protein |
| 4 | 18 | 29.5 | 10 | 2 | A60589 | spectrin-activating P |
| 5 | 17 | 27.9 | 8 | 2 | A05169 | neuropeptide M-I - |
| 6 | 17 | 27.9 | 10 | 2 | A37268 | IG heavy chain C r |
| 7 | 17 | 27.9 | 12 | 2 | S21205 | IG heavy chain V r |
| 8 | 17 | 27.9 | 12 | 2 | PH1187 | T-cell receptor al |
| 9 | 16 | 26.2 | 7 | 2 | A46868 | alpha-myosin heavy |
| 10 | 16 | 26.2 | 9 | 2 | G58502 | kidney and bladder |
| 11 | 16 | 26.2 | 10 | 2 | UC1416 | hypertrehalosemic |
| 12 | 16 | 26.2 | 10 | 2 | S09138 | hypertrehalosemic |
| 13 | 16 | 26.2 | 11 | 2 | A32428 | amine oxidase (cop |
| 14 | 15 | 24.6 | 7 | 2 | S29735 | polyphosphate-gluc |
| 15 | 15 | 24.6 | 9 | 2 | PT0231 | IG heavy chain CDR |
| 16 | 15 | 24.6 | 9 | 2 | A56029 | N-methylpurine DNA |
| 17 | 15 | 24.6 | 10 | 2 | S33844 | alpha-2-macroglobu |
| 18 | 15 | 24.6 | 10 | 2 | S27873 | hypothetical prote |
| 19 | 15 | 24.6 | 10 | 2 | S38304 | lectin GNL1 alpha |
| 20 | 15 | 24.6 | 11 | 2 | A38841 | rhodopsin homolog |
| 21 | 15 | 24.6 | 11 | 2 | S35490 | type II site-speci |
| 22 | 15 | 24.6 | 12 | 2 | PH1190 | T-cell receptor al |
| 23 | 15 | 24.6 | 12 | 2 | S51737 | T-cell receptor be |
| 24 | 14 | 23.0 | 4 | 2 | A35779 | neuropeptide Antho |
| 25 | 14 | 23.0 | 7 | 2 | UN0859 | peptidyl-di-peptida |
| 26 | 14 | 23.0 | 7 | 2 | S78024 | ribosomal protein |
| 27 | 14 | 23.0 | 8 | 2 | S08995 | hypertrehalosemic |
| 28 | 14 | 23.0 | 8 | 2 | A49823 | adipokinetic hormo |
| 29 | 14 | 23.0 | 8 | 2 | A44960 | neuropeptide led-C |

| | | | | | | |
|----|----|------|----|---|--------|--------------------|
| 30 | 14 | 23.0 | 9 | 2 | PM0002 | chlorophyll a/b-bi |
| 31 | 14 | 23.0 | 9 | 2 | S13636 | coat protein beta |
| 32 | 14 | 23.0 | 9 | 2 | PM0238 | IG heavy chain CRD |
| 33 | 14 | 23.0 | 10 | 1 | SEPGNK | neuremedin K - pig |
| 34 | 14 | 23.0 | 10 | 2 | C61033 | ranatichykinin C - |
| 35 | 14 | 23.0 | 10 | 2 | B46453 | e antigen p20 pre |
| 36 | 14 | 23.0 | 10 | 2 | S70251 | nucleoside (EC 1. |
| 37 | 14 | 23.0 | 11 | 2 | B41835 | translation elonga |
| 38 | 14 | 23.0 | 11 | 2 | S19301 | endo-1,4-beta-xyla |
| 39 | 14 | 23.0 | 11 | 2 | PM0028 | protein OA00042 - |
| 40 | 14 | 23.0 | 11 | 2 | S60354 | retinal oxidase - |
| 41 | 14 | 23.0 | 11 | 2 | S53436 | beta-D-galactosida |
| 42 | 14 | 23.0 | 11 | 2 | PM0904 | T-cell receptor be |
| 43 | 14 | 23.0 | 12 | 1 | A43975 | locustamyotropin - |
| 44 | 14 | 23.0 | 12 | 2 | S25485 | transcription fact |
| 45 | 14 | 23.0 | 12 | 2 | S71034 | potB protein - Sal |

ALIGNMENTS

RESULT 1

S28055 cytochrome b559 component psbf - pepper chloroplast (fragment)

C/Species: chloroplast Capsicum annuum (pepper)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jun-1999

C/Accession: S28055

R/Kurtz, M.; Camara, B.; Weill, J.H.; Schantz, R.

Plant Mol. Biol. 20, 1185-1188, 1992

A/Title: The psbf gene from bell pepper (Capsicum annuum): psbfid RNA editing also occurs

A/Reference number: S28055, MUID:93099270, PMID:1463853

A/Accession: S28055

A/Molecule type: DNA

A/Residues: 1-10 <KUN>

A/Cross-references: EMBL:X65570; NID:G14344; PIDN:CAA46539.1; PID:G415734

A/Genes: psbf

A/Genome: chloroplast

A/Superfamily: cytochrome b559 component F

C/Keywords: chloroplast, photosynthesis, photosystem II, thylakoid

Query Match

Best Local Similarity 37.7%; Score 23; DB 2; Length 10;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFM 8
DB 1 SISAWQFI 8

RESULT 2

A58718 carotenoid U149 - Carnobacterium sp. (fragment)

C/Species: Carnobacterium sp.

C/Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998

C/Accession: A58718

R/Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.

Appl. Environ. Microbiol. 58, 1417-1422, 1992

A/Title: Purification and characterization of a new bacteriocin isolated from a Carnobac

A/Reference number: A58718, MUID:92321768, PMID:1622206

A/Accession: A58718

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-7 <STO>

C/Keywords: antibiotic, lanthionine

Query Match 29.5%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6
DB 2 SEIQ 5

RESULT 3
S78420
ribosomal protein RL41, mitochondrial [validated] - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C/Accession: S78420
R/Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A/Reference number: S78411
A/Accession: S78420
A/Molecule type: protein
A/Residues: 1-9 <GOL>
A/Note: the protein is designated as mitochondrial ribosomal protein L41
C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 29.5%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12
Db 5 HRLG 8

RESULT 4
A60589
sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchi
C/Species: Heterocentrotus mamillatus
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C/Accession: A60589
R/Ioshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, Y.
Comp. Biochem. Physiol. B 94, 739-751, 1989
A/Title: A halogenated amino acid-containing sperm activating peptide and its related peptidic nucleus, Echinometra mathaei and Heterocentrotus mamillatus.
A/Reference number: A60527
A/Accession: A60589
A/Molecule type: protein
A/Residues: 1-10 <YOS>
C/Keywords: unassigned animal peptides

Query Match 29.5%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNLG 12
Db 2 YNLG 5

RESULT 5
A05169
neuropeptide M-I - American cockroach
C/Species: Periplaneta americana (American cockroach)
C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993
C/Accession: A05169
R/Willem, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A/Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry.
A/Reference number: A90118; MUID:85046530; PMID:6548628
A/Accession: A05169
A/Molecule type: protein
A/Residues: 1-8 <MIT>
C/Keywords: neuropeptide

Query Match 27.9%; Score 17; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 EIQFMHN 10
Db 1 EVNFSN 7

RESULT 6
A37268
Ig heavy chain C region (I29) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C/Accession: A37268
R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenny Jr., J.R.
J. Biol. Chem. 266, 5607-5613, 1991
A/Title: Heavy and light chain variable region sequences and antibody properties of anti-
A/Reference number: A3740; MUID:91177923; PMID:1706720
A/Accession: A37268
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-10 <RUF>

Query Match 27.9%; Score 17; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 3.1e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMHN 12
Db 1 ESQSFNVG 9

RESULT 7
S21205
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C/Accession: S21205
R/Makiya, R.; Stigbrand, T.
Eur. J. Biochem. 205, 341-345, 1992
A/Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin-C
A/Reference number: S21205; MUID:92209522; PMID:155592
A/Accession: S21205
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-12 <MAK>
C/Keywords: heterotetramer; immunoglobulin

Query Match 27.9%; Score 17; DB 2; Length 12;
Best Local Similarity 33.3%; Pred. No. 3.8e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 EIQFMHN 12
Db 1 EVOLVESG 9

RESULT 8
PH187
T-cell receptor alpha chain V region (Cw3/1P11) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH187
R/Casanova, J.; Cecotini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Widge, J.
Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor.
A/Reference number: S6512; MUID:92364546; PMID:1380061
A/Accession: PH187
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>

Query Match 27.9%; Score 17; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIOF 7
Db 2 AVSENGF 8

```

RESULT 9
146868
alpha-myosin heavy chain - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C/Accession: 146868
R.Friedman, D.J.; Umegaki, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricular
A/Reference number: 146868; MUID:84221901; PMID:6328491
A/Accession: 146868
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-7 <PRT>
A/Cross-references: GB:K01698; NID:9165538; PIDN:AA31415.1; PID:9165539

Query Match
26.2%; Score 16; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Gaps 0; Indels 0;

QY 6 QFMNH 10
| | |
| | |
Db 1 QFMNH 5

RESULT 10
G58502
kidney and bladder stone protein - unidentified bacterium (fragment)
C/Species: unidentified bacterium
C/Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C/Accession: G58502
R.Binet, J.P.; Binette, M.B.
Submitted to the Protein Sequence Database, October 1996
A/Description: The proteins of kidney and gallbladder stones.
A/Reference number: A58501
A/Accession: G58502
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <BIN>
A/Experimental source: human kidney stone, bladder stone
A/Note: a secondary sequence AAKENPKD was also found

Query Match
26.2%; Score 16; DB 2; Length 9;
Best Local Similarity 28.6%; Pred. No. 2.8e+05;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYSEIOF 7
| | | |
| | | |
Db 1 SLPVXF 7

RESULT 11
JC1416
hypertrehalosemic hormone I - stick insect (Carausius morosus)
N/Alternate names: neuropeptide Cam-HrTH-I
N/contains: hypertrehalosemic factor II
C/Species: Carausius morosus
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: JC1416; S07157
R.Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992
A/Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick in
A/Reference number: JC1416; MUID:93129188; PMID:1482345
A/Accession: JC1416
A/Molecule type: protein
A/Residues: 1-10 <GAE1>
R.Gaede, G.; Rinehart Jr., K.L.
Biol. Chem. Hoppe-Seyler 368, 67-75, 1987
A/Title: Primary structure of the hypertrehalosemic factor II from the corpus cardiacum
A/Reference number: S07157; MUID:87157103; PMID:3828078
A/Accession: S07157

A/Molecule type: protein
A/Residues: '2', 2-10 <GAE2>
C/Comment: Hypertrehalosemic factor II lacks the tryptophan modification.
C/Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplanet
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic aci
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/8/Binding site: carboxylate (Trp) (covalent) #status experimental
F/10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match
26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 4.8e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMNLG 12
| | | | |
| | | | |
Db 1 QLFTFPMWG 9

RESULT 12
S09138
hypertrehalosemic hormone II - stick insect (Exotosoma tiaratum)
N/Alternate names: Cam-HrTH-II
C/Species: Exotosoma tiaratum
C/Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C/Accession: S09138
R.Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora
entellae and of the stick insect Exotosoma tiaratum assigned by tandem fast atom bombard
A/Reference number: S08995; MUID:90253659; PMID:2340112
A/Accession: S09138
A/Molecule type: protein
A/Residues: 1-10 <GAE>
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match
26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 4.8e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMNLG 12
| | | | |
| | | | |
Db 1 QLFTFPMWG 9

RESULT 13
A32428
amine oxidase (copper-containing) (EC 1.4.3.6) - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 06-Sep-1996
C/Accession: A32428
R.van der Meer, R.A.; van Wassenaar, P.D.; van Brouwerhaven, J.H.; Duine, J.A.
Biochem. Biophys. Res. Commun. 159, 726-733, 1989
A/Title: Primary structure of a pyrroloquinoline quinone (PQQ) containing peptide isolat
A/Reference number: A32428; MUID:89193662; PMID:2539124
A/Accession: A32428
A/Molecule type: protein
A/Residues: 1-7, 'K', 9-11 <VAN>
A/Note: the modified residue thought by the authors to be pyrroloquinoline quinone coval
C/Keywords: oxidoreductase; quinoprotein; topaquinone
F/8/Modified site: topaquinone (Tyr) #status predicted

Query Match
26.2%; Score 16; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 5.3e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 SEIQFMNH 10
| | | |
| | | |
Db 2 SDAVFYIN 9
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Tue May 18 12:03:04 2004

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Page 4

RESULT 14

S29735
polyphosphate-glucose phosphotransferase (EC 2.7.1.63) - *Propionibacterium freudenreichii*
C:Species: *Propionibacterium freudenreichii* subsp. *shermanii*
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
C:Accession: S29735
R:Phillips, N.F.B.; Horn, P.J.; Wood, H.G.
Arch. Biochem. Biophys. 300, 309-319, 1993
A:Title: The polyphosphate- and ATP-dependent glucokinase from *Propionibacterium shermanii*
A:Reference number: S29735; MUID:9314332; PMID:8380966
A:Accession: S29735
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <PHI>
C:Keywords: phosphotransferase

Query Match 24.6%; Score 15; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 HNLG 12
| | |
Db 2 HVLG 5

RESULT 15

PT0231
Ig heavy chain CDR3 region (clone 1-118B) - human (fragment)
C:Species: *Homo sapiens* (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0231
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:9108337; PMID:1899102
A:Accession: PT0231
A:Molecule type: DNA
A:Residues: 1-9 <IAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 24.6%; Score 15; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 7 FMHNLG 12
: | : |
Db 1 YTHSEG 6

Search completed: May 18, 2004, 10:05:40
Job time : 10.25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:43:45 ; Search time 6.75 Seconds
(without alignments)
92.569 Million cell updates/sec

Title: US-09-730-174A-4
Perfect score: 61
Sequence: 1 SVSEIOPFMNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|-----------------|---------------------|
| 1 | 23 | 37.7 | 10 1 PSBF_CAPAN | O03367 capsicum an |
| 2 | 18 | 29.5 | 7 1 LANC_CARUT | P36960 carinabacter |
| 3 | 18 | 29.5 | 10 1 HTPL_ROMMI | P18110 romalea mic |
| 4 | 16 | 26.2 | 8 1 ALP6_CYPDO | P82157 cydia pomon |
| 5 | 16 | 26.2 | 10 1 HTF2_CARMO | P11385 carausius m |
| 6 | 15 | 24.6 | 5 1 EIO3_LITRU | P82099 litoria rub |
| 7 | 15 | 24.6 | 8 1 FUS8_FUSGO | P81010 fusarium so |
| 8 | 15 | 24.6 | 10 1 RPL1_PRODV | P35946 phosine dis |
| 9 | 15 | 24.6 | 11 1 BRG_CLOPA | P81350 chlostridium |
| 10 | 15 | 24.6 | 11 1 NDMH_CANFA | P49820 canis fam11 |
| 11 | 15 | 24.6 | 11 1 T2P1_PROVU | P31031 proteus vul |
| 12 | 14 | 23.0 | 4 1 FLRN_ANTEL | P58707 anthopleura |
| 13 | 14 | 23.0 | 7 1 ALI7_CYPDO | P82158 cydia pomon |
| 14 | 14 | 23.0 | 7 1 TV51_LITRU | P82065 litoria rub |
| 15 | 14 | 23.0 | 8 1 ALI8_CARMA | P81821 carcinus ma |
| 16 | 14 | 23.0 | 8 1 ALI1_CYPDO | P82152 cydia pomon |
| 17 | 14 | 23.0 | 8 1 HTF1_PERAM | P04548 periplaneta |
| 18 | 14 | 23.0 | 9 1 FAR8_MACRS | P83881 macrobrachi |
| 19 | 14 | 23.0 | 9 1 UF02_MOUSE | P38640 mus musculu |
| 20 | 14 | 23.0 | 10 1 ALI3_CARMA | P81822 carcinus ma |
| 21 | 14 | 23.0 | 10 1 TRNC_RANCA | P22690 rana catesb |
| 22 | 14 | 23.0 | 10 1 TRNK_PIG | P01392 sus scrofa |
| 23 | 14 | 23.0 | 11 1 ASL1_BACSE | P83146 bacteroides |
| 24 | 14 | 23.0 | 12 1 HCV1_CARMA | P83176 carcinus ma |
| 25 | 14 | 23.0 | 12 1 LMT1_LOCMI | P22395 locusta mig |
| 26 | 14 | 23.0 | 12 1 FORD_METIM | P80903 metanabact |
| 27 | 14 | 23.0 | 12 1 RS19_TOBBP | O56251 tomato big |
| 28 | 13 | 21.3 | 6 1 TRP1_PSEPU | P25414 pseudomonas |
| 29 | 13 | 21.3 | 8 1 HTP1_TENNO | P25519 tenebrio mo |
| 30 | 13 | 21.3 | 8 1 LCK4_LEUMA | P21143 leucophaea |
| 31 | 13 | 21.3 | 8 1 LCK6_LEUMA | P19988 leucophaea |
| 32 | 13 | 21.3 | 9 1 CONO_CONGE | P05486 conus geogr |
| 33 | 13 | 21.3 | 9 1 MOSH_CLYJA | P19952 clypeaster |

| | | | | |
|----|----|------|-----------------|--------------------|
| 34 | 13 | 21.3 | 9 1 OXY1_EISFO | P42998 eisenia foe |
| 35 | 13 | 21.3 | 9 1 PPX1_PERAM | P82691 periplaneta |
| 36 | 13 | 21.3 | 11 1 ASL2_BACSE | P83147 bacteroides |
| 37 | 13 | 21.3 | 11 1 COR2_PERAM | P11495 periplaneta |
| 38 | 13 | 21.3 | 11 1 CSIS_BACSV | P81095 bacillus su |
| 39 | 13 | 21.3 | 11 1 PVK1_PERAM | P41837 periplaneta |
| 40 | 13 | 21.3 | 11 1 O2O3_COMTE | P80464 comanana t |
| 41 | 13 | 21.3 | 12 1 UKA2_HUMAN | P31144 homo sapien |
| 42 | 13 | 21.3 | 12 1 UR2_FOLSP | P81022 polyodon sp |
| 43 | 12 | 19.7 | 5 1 RE21_LITRU | P82071 litoria rub |
| 44 | 12 | 19.7 | 5 1 RE31_LITRU | P82072 litoria rub |
| 45 | 12 | 19.7 | 8 1 ANG2_BOTJA | Q10582 bochrops ja |

ALIGNMENTS

RESULT 1

PSBF_CAPAN STANDARD; PRT; 10 AA.

ID PSBF_CAPAN
AC O03367;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI)
DE (Fragment).
GN PSBF
OS Capsicum annuum (Bell pepper).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID:4072.
[1]

RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lamuyo; TISSUE=fruit, and leaf;
RX MEDLINE=93099270; PubMed=1463853;
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;
RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA
editing also occurs in non-photosynthetic chromoplasts.";
RT Plant Mol. Biol. 20:1185-1188(1992).
RL
CC -!- FUNCTION: This b-type cytochrome is tightly associated with the
CC reaction center of photosystem II and possibly is part of the
CC water-oxidation complex.
CC -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC -!- SIMILARITY: Belongs to the psbL / psbF family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).

DR EMBL, X65570; CAA46539.1; -.
DR PIR, S28055; S28055.
DR HAMAP, MF_00643; -? 1.
DR InterPro, IPR006216; Cyt_b559.
DR PROSITE, PS00537; CYTOCHROME B559; PARTIAL.
KW Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT NOW TRF 1
FT TRANSMEM <1 5
FT DOMAIN 6 10
SQ SEQUENCE 10 AA; 1180 MW; 817D0F59D6D6DC5 CRC64;

Query Match 37.7%; Score 23; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1,2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 SVSEIOPFM 8
| : : : : :
Db 1 SISAMQPI 8

```
RESULT 2
LANC_CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 28, Created)
DT 01-JUN-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lanthibiotic caruocin U149 (Fragment).
OS Carnobacterium sp. (strain U149).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
CC Carnobacterium.
NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RL a Carnobacterium sp."
CC Appl. Environ. Microbiol. 58:1417-1422(1992).
DE -1- FUNCTION: Lanthionine-containing peptide antibiotic (lanthibiotic).
CC Active on Gram-positive bacteria.
KW Antibiotic; Bacteriocin; Lanthibiotic.
FT NON TER
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match
Best Local Similarity 29.5%; Score 18; DB 1; Length 7;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIO 6
DB 2 SEIO 5

RESULT 3
HTF1_ROMMI STANDARD; PRT; 10 AA.
AC P1185;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RO I (Hypertrehaloseamic factor).
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthoptera; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
NCBI_TaxID=7007;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuuropeptides of the ACH/RPCH-family from
RT the lubber grasshopper, Romalea microptera."
RL Peptides 9:681-688(1988).
DE -1- FUNCTION: Hypertrehaloseamic factors are neuuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the ACH / HPTH / RPCH family.
DR InterPro; IPR002047; ACH.
DR PROSITE; PS00256; ACH; 1.
KW Neuuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1
FT MOD RES 10 10 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1163 MW; 056236745711A9C4 CRC64;

Query Match
Best Local Similarity 29.5%; Score 18; DB 1; Length 10;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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QY 4 EIOFMHNG 12
DB 1 QVNFTRNG 9

RESULT 4
ALB6_CYPDO STANDARD; PRT; 8 AA.
ID ALB6_CYPDO
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydia pomonella (Codling moth).
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RX TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Davey H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily."
RL Peptides 18:1301-1309(1997).
DE -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuuropeptide; Amidation.
FT MOD RES 8 8
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match
Best Local Similarity 26.2%; Score 16; DB 1; Length 8;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MHNG 12
DB 3 LYNFG 7

RESULT 5
HTF2_CARMO STANDARD; PRT; 10 AA.
ID HTF2_CARMO
AC P1185;
DT 01-JUL-1999 (Rel. 11, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehaloseamic factor II (HTF-II) (HPTH-II) (Hypertrehaloseamic
DE neuuropeptide II).
OS Carausius morosus (Indian stick insect), and
OS Exaltosoma tiaratum (Stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatoidea; Euphasmida; Phasmatoidea;
OC Heteromelidae; Carausius.
OX NCBI_TaxID=7022, 7024;
RN [1]
RP SEQUENCE.
RX SPECIES=C. morosus; TISSUE=Corpora cardiaca;
RX MEDLINE=87157103; PubMed=3828078;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structure of the hypertrehaloseamic factor II from the
RT corpus cardiaca of the Indian stick insect, Carausius morosus,
RT determined by fast atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN [2]
RP SEQUENCE.
RX SPECIES=E. tiaratum; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehaloseamic neuuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Grylloblatta campodeiformis, Blattella germanica and Blattella orientalis
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RT and of the stick insect Extracoma tatarum assigned by tandem fast
RT atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RC CARBOHYDRATE-LINKAGE SITE.
RC SPECIES=C. morosus; TISSUE=Corpora cardiaca;
RA MEDLINE=91129188; PubMed=1482345;
RA Gaede G., Keilner R., Rinehart K.L. Jr., Proefke M.L.;
RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT a stick insect corpus cardiaca."
RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC -1- FUNCTION: Hypertrahaloase factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1308.61; METHOD=FAH.
CC -1- SIMILARITY: Belongs to the AKH / HPTH / RPCH family.
DR PIR: J01416; J01416.
DR PIR: S09138; S09138.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).
FT MOD_RES 10 10 AMIDATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A5D1 CRC64;

Query Match 26.2%; Score 16; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 2.7e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 4 EIOFMHNLG 12
DB 1 QLTFTPNWG 9

RESULT 6
EIO3 LITRU STANDARD; PRT; 5 AA.
AC P82059;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodytidae; Litoria.
OC NCB1_TaxID=104895;
RN [1]
RP SEQUENCE.
RP TISSUE=Skin secretion;
RA Mahnir P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 5 AMIDATION.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A0000 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FMH 9
DB 1 FVH 3

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FUS3_FUSO STANDARD; PRT; 8 AA.
ID FUS3_FUSO
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Allergen Fus 8 13596* (Fragment).
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCB1_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma U., Gangal S.V.;
RL Submitted (JUL-1997) to Swiss-Prot.
CC -1- ALLERGEN: Causes an allergic reaction in human.
KW Allergen.
FT NON_TER 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 HNL 11
DB 5 HNV 7

RESULT 8
ID RPL_PRODV STANDARD; PRT; 10 AA.
AC P35946;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (large structural protein)
DE (L protein) (Fragment).
GN L.
OS Phocine distemper virus (PDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCB1_TaxID=11240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U13ref/89;
RX MEDLINE=92268877; PubMed=1588321;
RA Curran M.D., O'Loan D., Kennedy S., Rima B.K.;
RT "Molecular characterization of phocine distemper virus: gene order
RT and sequence of the gene encoding the attachment (H) protein."
RL J. Gen. Virol. 73:1189-1194(1992).
CC -1- FUNCTION: Probable component of the active polymerase. It may
CC function in mRNA synthesis, capping, methylation and poly(A)
CC synthesis of newly synthesized viral mRNAs. RNA editing of the P
CC gene transcript, and protein kinase activity.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate +
CC (RNA) (N).
CC -1- SIMILARITY: Belongs to the paramyxoviruses L protein family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL: D10371; BAA01208.1; -
KW Transferase; RNA-directed RNA polymerase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;

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RESULT 7

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Query Match      24.6%; Score 15; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEI 5
   ||:|
   5 SVNOI 9

Db

RESULT 9
ID_EFG_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUS1.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=MS;
RX MEDLINE=98291870; PubMed=9629918;
RA Flanagan R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum MS.";
RI Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
the nascent protein chain from the A-site to the P-site of the
ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro: IPR000795; EF_Grpbind.
KW Elongation factor; Protein biosynthesis; GTP-binding.
RN NON_TER 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match      24.6%; Score 15; DB 1; Length 11;
Best Local Similarity 25.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 IQFMHNG 12
   ||:|
   4 LEKFNQIG 11

Db

RESULT 10
ID_NDUM_CANPA STANDARD; PRT; 11 AA.
AC P49820;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Fragment).
GN NDUFV2.
OS Carls famliaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins";
RI Electrophoresis 18:2795-2802(1997).

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CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FS)
FRAGMENT OF THE ENZYME.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COFACTOR: Binds 1 2Fe-2S cluster (potential).
CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
DR HSC-2DPAGE; P49820; DOG.
DR InterPro: IPR002023; Cmplx1_24kDa.
DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
KW Iron-sulfur; Iron; 2Fe-2S.
RN NON_TER 11
SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match      24.6%; Score 15; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.7e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FVH 9
   ||:|
   7 FVH 9

Db

RESULT 11
ID_T2P1_PROVU STANDARD; PRT; 11 AA.
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Type II restriction enzyme PvuII (EC 3.1.21.4) (Endonuclease PvuII)
DE (R.PvuII) (Fragment).
GN PvuII.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 13315;
RX MEDLINE=93087186; PubMed=1454536;
RA Smith W.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvuII restriction and
RT modification system.";
RI Nucleic Acids Res. 20:5743-5747(1992).
CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CLEAVES AFTER T-4.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
specific double-stranded fragments with terminal 5'-phosphates.
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DR EMBL; L04163; AAA25660.1; -
DR PIR; S35490; S35490.
DR REBASE; 1541; PvuII.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
RN NON_TER 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match      24.6%; Score 15; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 SYSEI 5
| | |
DB 2 SYDEL 6

RESULT 12

FLRN ANTEL STANDARD; PRT; 4 AA.
ID FLRN ANTEL
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nymathea; Actinellidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RX Grimmelikhuisen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reischneider R.K., Nohacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenylalanyl-Leu-Arg-Asn-NH₂ (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group."
RT Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
RL -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron specific.
CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAE.
DR PIR: A35779; A35779.
KM Neuropeptide; Amidation.
FT MOD_RES 1 4 L-3-PHENYLLACTYL.
FT MOD_RES 1 1 AMIDATION.
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 EXEN 10
| | |
DB 1 FLRN 4

RESULT 13
AL7 CYDPO STANDARD; PRT; 7 AA.
ID AL7 CYDPO
AC P82158;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 7.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Platyraia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Duvé H., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily."
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
KM Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 873 MW; 672879CAB8569350 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 8 MENIG 12
| | |
DB 2 MIDFG 6

RESULT 14

TY51 LITRU STANDARD; PRT; 7 AA.
ID TY51 LITRU
AC P82065;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tytophyllin 5.1.
OS Litorea rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litorea.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion.
RX Seibomner S.T., Mabiniz P.A., Maugh R.J., Bowie J.R., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litorea rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians."
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=965; METHOD=FAE.
KM Amphibian defense peptide; Amidation; Neuropeptide;
KM Pyrolidone carboxylic acid.
FT MOD_RES 1 7 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 7 AMIDATION.
SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 EIOFWH 9
| | |
DB 1 QIPWFH 6

RESULT 15
AL18 CARVA STANDARD; PRT; 8 AA.
ID AL18 CARVA
AC P81821;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 18.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaroš P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -1- SIMILARITY: Belongs to the allatostatin family.
KM Neuropeptide; Amidation; Multigene family.

Tue May 18 12:03:04 2004

us-09-730-174a-4.closed.rsp

Page 6

FT MOD RES 8 8 AMIDATION (POTENTIAL).
SQ SEQUENCE 8 AA; 919 MW; C82879D5A5659AB5 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 8 MHNLG 12
|:|
Db 3 MYSFG 7

Search completed: May 18, 2004, 10:02:34
Job time : 7.75 secs

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Thymidylate synthase (Fragment).
 GN TS.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21015404; PubMed=11130975;
 RA Brouillette J.A., Andrew J.R., Vonta P.J.;
 RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
 RT method.";
 RL Mamm. Genome 11:1079-1086(2000).
 DR EMBL; AF202073; AAF20918.1; -.
 FT NON TER 1 1
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 899 MW; 6731A1E059C9A867 CRC64;

 Query Match 31.1%; Score 19; DB 6; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 FHENL 11
 DB 4 FHTL 8

 RESULT 3
 ID 092766 PRELIMINARY; PRT; 9 AA.
 AC 092766;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE Fusion protein (Fragment).
 GN F.
 OS Canine distemper virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 NCBI_TaxID=11232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dog #5526/89;
 RA Liernum H., Harder T., Haas L.;
 RT "Genetic analysis of the central untranslated genome region and the
 RT proximal coding part of the F gene of wild-type and vaccine distemper
 RT morbilliviruses.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF026237; AAC09167.1; -.
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1011 MW; F28173276053441 CRC64;

 Query Match 31.1%; Score 19; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 10
 DB 1 MHN 3

 RESULT 4
 ID 071066 PRELIMINARY; PRT; 9 AA.
 AC 071066;
 DT 01-AUG-1998 (TReMBLrel. 07, Created)
 DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Fusion protein (Fragment).
 GN F.
 OS Canine distemper virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 NCBI_TaxID=11232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dog #10757/96;
 RA Liernum H., Harder T., Haas L.;
 RT "Genetic analysis of the central untranslated genome region and the
 RT proximal coding part of the F gene of wild-type and vaccine distemper
 RT morbilliviruses.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF026234; AAC09164.1; -.
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1124 MW; F29D04576044041 CRC64;

 Query Match 31.1%; Score 19; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 10
 DB 1 MHN 3

 RESULT 5
 ID P82081 PRELIMINARY; PRT; 12 AA.
 AC P82081;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE DYNASTIN 3.
 OS Limnodynastes terraereginae (Northern Banjo frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Limnodynastinae; Limnodynastes.
 NCBI_TaxID=104894;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=IBIDIAL GLAND;
 RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structure of the dynastins from
 RT the banjo frogs Limnodynastes terraereginae, Limnodynastes dumerilii and
 RL Limnodynastes terraereginae.";
 RL Aust. J. Chem. 46:833-842(1993).
 CC -1- MASS SPECTROMETRY: MW=1236; METHOD=FA5.
 SQ SEQUENCE 12 AA; 1236 MW; 147AA70FDF472724 CRC64;

 Query Match 31.1%; Score 19; DB 13; Length 12;
 Best Local Similarity 60.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 12
 DB 7 LNNIG 11

 RESULT 6
 ID 013591 PRELIMINARY; PRT; 8 AA.
 AC 013591;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE ORF YN1337M (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Obermaier B., Piravandi E., Rinke M.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z1612; CAA96271.2; -.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 1005 MW; 5CA441E449C9720 CRC64;
 Query Match 29.5%; Score 18; DB 3; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 FMHN 10
 DB 4 FMHN 7
 RESULT 7
 Q15342 PRELIMINARY; PRT; 10 AA.
 AC Q15342;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Aml1 protein (Fragment).
 GN AML1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96226397; PubMed=8634147;
 RA Levanon D., Bernstein Y., Negreanu V., Ghozi M.C., Bar-Am I.,
 RA Aloya R., Goldenberg D., Lotem J., Groner Y.,
 RT "A large variety of alternatively spliced and differentially expressed
 RT mRNAs are encoded by the human acute myeloid leukemia gene AML1.",
 RL DNA Cell Biol. 15:175-185 (1996).
 DR EMBL; X90978; CAA62465.1; -.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1254 MW; 8D99287B441AF365 CRC64;
 Query Match 29.5%; Score 18; DB 4; Length 10;
 Best Local Similarity 44.4%; Pred. No. 8.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 SVSEIOFMH 9
 DB 1 SVSWXRYPH 9
 RESULT 8
 Q8M50 PRELIMINARY; PRT; 12 AA.
 AC Q8M50;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Anoda cristata.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Malvales; Malvaceae; Malvoideae; Anoda.
 OX NCBI_TaxID=193227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Preil B.B., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl6 intron.",
 RL Syst. Bot. 27:333-350 (2002).
 DR EMBL; AF384867; AA050405.1; -.
 GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
 FT NON_TER 1
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1431 MW; 9A5E5B65452C9CA CRC64;
 Query Match 29.5%; Score 18; DB 8; Length 12;
 Best Local Similarity 37.5%; Pred. No. 1.1e+04;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 4 EIOFMHN 11
 DB 3 EPDFVNNI 10
 RESULT 9
 Q85631 PRELIMINARY; PRT; 12 AA.
 AC Q85631;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE MH2, proviral DNA, myc to 3' LTR (Fragment).
 OS Avian carcinoma virus.
 OC Viruses; Retroviridae; Retroviridae; Alpharetrovirus.
 OX NCBI_TaxID=11958;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85033920; PubMed=6092695;
 RA Suttrave P., Jansen H.W., Bister K., Rapp U.R.;
 RA "3'-terminal region of avian carcinoma virus MH2 shares sequence
 RT elements with avian sarcoma viruses Y73 and SR-A.",
 RL J. Virol. 52:703-705 (1984).
 DR EMBL; K03100; AAA44238.1; -.
 FT NON_TER 1
 SQ SEQUENCE 12 AA; 1466 MW; 72E4B884F30736DB CRC64;
 Query Match 29.5%; Score 18; DB 15; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 HNL 11
 DB 2 HNL 4
 RESULT 10
 Q23876 PRELIMINARY; PRT; 11 AA.
 AC Q23876;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
 DE Actin 4.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelidida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82260445; PubMed=6286214;
 RA McKewen M., Firtel R.A.;
 RA "Actin multigene family of Dictyostelium.",
 RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505 (1982).
 DR EMBL; K02957; AAA33150.1; -.
 GO; GO:0009507; C:chloroplast; IEA.
 Query Match 27.9%; Score 17; DB 5; Length 11;
 Best Local Similarity 28.6%; Pred. No. 1.5e+04;
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 4 EIOFMHN 10
 DB 5 DVQALNN 11

RESULT 11

Q35374 ID 035374 PRELIMINARY; PRT; 11 AA.
 AC 035374;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE PI protein (Fragment).
 OS Paramacium tetraurelia.
 OG Microchondrion.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
 OC Paramacium.
 OC NCBI_TaxID=5888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=stock 172;
 RX MEDLINE=87055241; PubMed=3023187;
 RA Pritchard A.E., Sellmer J.J., Cummings D.J.;
 RT "Paramacium mitochondrial DNA sequences and RNA transcripts for
 RT cytochrome oxidase subunit I, URF1, and three ORFs adjacent to the
 RT replication origin."
 RL Gene 44:243-253(1986).
 DR EMBL: M5280; AAA79267.1; -;
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KN Mitochondrion.
 FT NON_TER
 FT SEQUENCE 11 AA; 1266 MW; 1D84259D16D046D4 CRC64;

Query Match 27.8%; Score 17; DB 8; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.5e+04;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSETQ 6
 DB 2 SLNQIQ 7

RESULT 12

Q28742 ID 028742 PRELIMINARY; PRT; 7 AA.
 AC 028742;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Alpha-myosin heavy chain (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84221901; PubMed=6328491;
 RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Okoyicic S.,
 RA Rabinowitz M.;
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-
 RT ventricular myosin heavy chains."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
 DR EMBL: K01698; AAA31415.1; -;
 DR PIR: I46868; I46868.
 FT NON_TER
 FT SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match 26.2%; Score 16; DB 6; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QFMEN 10
 DB 1 QXMPD 5

RESULT 13

Q8UJ20 ID 08UJ20 PRELIMINARY; PRT; 7 AA.
 AC 08UJ20;
 DT 01-OCT-2002 (TRENBLREL. 22, Created)
 DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
 DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
 DE Extracellular fatty acid binding protein (Fragment).
 GN EXFABP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Wang Q., Li N., Li H.;
 RT "Cloning and sequencing of 3' UTR of EXFABP gene in chicken."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF487519; AA19665.1; -;
 FT NON_TER
 FT SEQUENCE 7 AA; 780 MW; 72CB1AB2D5BEB370 CRC64;

Query Match 26.2%; Score 16; DB 13; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSET 5
 DB 3 SVDEV 7

RESULT 14

Q05403 ID 005403 PRELIMINARY; PRT; 8 AA.
 AC 005403;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
 DE DNA for ORF 5 from chromosome XV (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FY1679;
 RX MEDLINE=96021609; PubMed=8533473;
 RA Zimmt E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
 RT "A 29,425 Kb segment on the left arm of yeast chromosome XV contains
 RT more than twice as many unknown as known open reading frames."
 RL Yeast 11:975-986(1995).
 DR EMBL: X83121; CAA58183.1; -;
 FT NON_TER
 FT SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 26.2%; Score 16; DB 3; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MENTL 11
 DB 2 INHV 5

RESULT 15

Q40659 ID 040659 PRELIMINARY; PRT; 8 AA.
 AC 040659;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)

DE Alpha-amylase (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91078641; PubMed=2258052;
RA Kumagai M.H., Shan M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA Rodriguez R.L.;
RT "Expression and secretion of rice alpha-amylase by saccharomyces
cerevisiae.";
RL Gene 94:209-216(1990).
DR EMBL; M62916; AAA33892.1; -.
DR Gramene; Q40659; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 948 MM; EBC69444732D6D6 CRC64;
QY 5 IQFMHNL 11
: : : : :
Db 1 MOVLINNM 7

Search completed: May 18, 2004, 10:04:47
Job time : 30.25 secs

Query Match 26.2%; Score 16; DB 10; Length 8;
Best Local Similarity 28.6%; Pred. No. 1e+06;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:42:39 ; Search time 45.75 Seconds
(without alignments)
74.111 Million cell updates/sec

Title: US-09-730-174A-4
Perfect score: 61
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 50 | 82.0 | 11 | 6 | ABG72607 |
| 2 | 50 | 82.0 | 12 | 6 | ABG72608 |
| 3 | 46 | 75.4 | 11 | 3 | AAV96968 |
| 4 | 45 | 73.8 | 10 | 2 | AAK1644 |
| 5 | 45 | 73.8 | 10 | 3 | AAV68767 |
| 6 | 45 | 73.8 | 10 | 4 | AAAB6219 |
| 7 | 45 | 73.8 | 10 | 6 | ABR4166 |
| 8 | 41 | 67.2 | 9 | 4 | AAAB6225 |
| 9 | 39 | 63.9 | 9 | 2 | AAK1645 |
| 10 | 39 | 63.9 | 9 | 3 | AAV96981 |
| 11 | 39 | 63.9 | 9 | 4 | AAAB6220 |
| 12 | 38.5 | 63.1 | 11 | 2 | AAV50600 |
| 13 | 36 | 59.0 | 9 | 3 | AAAB1862 |
| 14 | 36 | 59.0 | 9 | 3 | AAV96966 |
| 15 | 33 | 54.1 | 9 | 3 | AAAB1863 |
| 16 | 33 | 54.1 | 10 | 4 | AAAB6932 |
| 17 | 33 | 54.1 | 11 | 4 | AAAB6931 |
| 18 | 33 | 54.1 | 11 | 4 | AAAB6915 |
| 19 | 33 | 54.1 | 11 | 4 | AAAB4770 |
| 20 | 33 | 54.1 | 12 | 4 | AAAB6914 |
| 21 | 33 | 54.1 | 12 | 4 | AAAB4769 |
| 22 | 32 | 52.5 | 9 | 3 | AAV78849 |
| 23 | 31 | 50.8 | 8 | 2 | AAAB1646 |
| 24 | 31 | 50.8 | 8 | 3 | AAAB7467 |
| 25 | 31 | 50.8 | 8 | 4 | AAAB6221 |

| | | | | | | |
|----|----|------|----|---|----------|--------------------|
| 26 | 31 | 50.8 | 10 | 6 | ABP71484 | ABP71484 Parathyro |
| 27 | 31 | 50.8 | 11 | 6 | ABP71485 | ABP71485 Parathyro |
| 28 | 31 | 50.8 | 11 | 6 | ABP71482 | ABP71482 Parathyro |
| 29 | 31 | 50.8 | 12 | 2 | AAW45785 | AAW45785 Parathyro |
| 30 | 31 | 50.8 | 12 | 6 | ABP71482 | ABP71482 Parathyro |
| 31 | 29 | 47.5 | 9 | 3 | AAAB1866 | AAAB1866 PTH(1-14) |
| 32 | 28 | 45.9 | 11 | 1 | AAAB2547 | AAAB2547 (asn10, T |
| 33 | 28 | 45.9 | 11 | 4 | AAAB6892 | AAAB6892 Rat parat |
| 34 | 28 | 45.9 | 12 | 4 | AAAB6891 | AAAB6891 Rat parat |
| 35 | 27 | 44.3 | 10 | 5 | ABG69386 | ABG69386 Vascular |
| 36 | 27 | 44.3 | 11 | 4 | ABU54029 | ABU54029 Human DNA |
| 37 | 26 | 42.6 | 6 | 2 | AAAB1648 | AAAB1648 Human par |
| 38 | 26 | 42.6 | 6 | 3 | AAV68764 | AAV68764 Amino aci |
| 39 | 26 | 42.6 | 6 | 4 | AAAB6223 | AAAB6223 Human par |
| 40 | 26 | 42.6 | 6 | 6 | ABR44168 | ABR44168 Human par |
| 41 | 26 | 42.6 | 7 | 2 | AAAB1647 | AAAB1647 Human par |
| 42 | 26 | 42.6 | 7 | 3 | AAAB0068 | AAAB0068 N-termina |
| 43 | 26 | 42.6 | 7 | 4 | AAAB6222 | AAAB6222 Human par |
| 44 | 26 | 42.6 | 9 | 3 | AAAB1864 | AAAB1864 PTH(1-14) |
| 45 | 26 | 42.6 | 9 | 3 | AAV97062 | AAV97062 PTH-xp N- |

ALIGNMENTS

| | | | |
|----------|--|------------------------------------|--|
| RESULT 1 | | ABG72607 standard; peptide; 11 AA. | |
| ID | ABG72607 | | |
| XX | ABG72607; | | |
| AC | 11-FEB-2003 (first entry) | | |
| DT | 11-FEB-2003 (first entry) | | |
| XX | Parathyroid hormone antigenic peptide 2-12. | | |
| DE | Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis; | | |
| XX | primary hyperparathyroidism; mouse; rat; bovine; porcine; canine. | | |
| KX | Homo sapiens. | | |
| XX | Mus sp. | | |
| OS | Rattus sp. | | |
| OS | Bos taurus. | | |
| OS | Sus scrofa. | | |
| OS | Canis familiaris. | | |
| XX | Key | Location/Qualifiers | |
| FT | Misc-difference 6 | /label= Leu, Phe | |
| FT | | | |
| XX | US2002110871-A1. | | |
| PV | 15-AUG-2002. | | |
| XX | 05-DEC-2000; 2000US-00730174. | | |
| PF | 05-DEC-2000; 2000US-00730174. | | |
| XX | 05-DEC-2000; 2000US-00730174. | | |
| PR | (ZABR/) ZABRADNIK R J. | | |
| XX | (LAVI/) LAVIGNE J R. | | |
| PA | Zahradnik RJ, Lavigne JR, | | |
| XX | WPI; 2003-066685/06. | | |
| DR | New parathyroid hormone (PTH) antigenic peptide inducing the formation | | |
| PT | and isolation of antibodies having an affinity to it; useful for | | |
| PT | detecting bioactive PTH levels in serum, plasma and/or cell culture | | |
| PT | media. | | |
| XX | Claim 1; Page 5; 11pg; English. | | |
| XX | The invention relates to a new antigenic peptide for inducing the | | |
| CC | formation and isolation of antibodies having an affinity to it, being | | |

CC formed from the N-terminus of parathyroid hormone (PTH). Also included
 CC are: (1) a method for producing antibodies useful in the determination of
 CC PTH levels in a biological sample comprising: (a) providing at least one
 CC first peptide antigen comprising a peptide fragment of PTH; (b)
 CC administering the first peptide antigen to a host animal to induce
 CC antibody production; (c) monitoring the antibody titre produced; (d)
 CC isolating antisera produced in the host animal; and (e) selecting
 CC antisera from the isolated antisera produced in the host that is capable
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by
 CC the method; and (3) test kits and analytical procedures used for the
 CC determination of bioactive intact PTH utilising (ab). The methods and
 CC compositions of the present invention are useful for determining
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
 CC The antigens, antibodies and methods of the present invention, as
 CC compared to prior art, have the particular advantages of possessing
 CC greater affinity for PTH, and in particular, are designed to have a novel
 CC recognition for amino acid residues extending beyond the first N-terminal
 CC PTH residue, and further have negligible cross-reactivity with the large
 CC non-molecular forms of PTH. PTH levels are an important parameter in
 CC patients suffering from hypercalcaemia, osteoporosis and primary
 CC hyperparathyroidism. The present sequence represents a PTH antigenic
 CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,
 CC canine and bovine PTH

SO Sequence 11 AA;

Query Match 82.0%; Score 50; DB 6; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.01;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 VSEIQFMNIG 12
 1 VSEIQFMNIG 11

Db

RESULT 2

ABG72608
 ID ABG72608 standard; peptide; 12 AA.

XX ABG72608;

DT 11-FEB-2003 (first entry)

DE Parathyroid hormone antigenic peptide 1-12.

XX Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
 KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.

XX Homo sapiens.

OS Mus sp.

OS Rattus sp.

OS Bos taurus.

OS Sus scrofa.

OS Canis familiaris.

XX Key

FT Misc-difference 1

FT Misc-difference 7

FT Misc-difference 7

XX US2002110871-A1.

XX 15-AUG-2002.

XX 05-DEC-2000; 2000US-00730174.

XX 05-DEC-2000; 2000US-00730174.

XX (ZAHAR/) ZAHARADNIK R J.

XX (LAVI/) LAVIGNE J R.

XX Zahradnik RJ, Lavigne JR;

PI

XX MPI; 2003-066685/06.
 DR New parathyroid hormone (PTH) antigenic peptide inducing the formation
 XX and isolation of antibodies having an affinity to it, useful for
 PT determining bioactive PTH levels in serum, plasma and/or cell culture
 PT media.
 PS Claim 2; Page 5; 11pp; English.

XX The invention relates to a new antigenic peptide for inducing the
 CC formation and isolation of antibodies having an affinity to it, being
 CC formed from the N-terminus of parathyroid hormone (PTH). Also included
 CC are: (1) a method for producing antibodies useful in the determination of
 CC PTH levels in a biological sample comprising: (a) providing at least one
 CC first peptide antigen comprising a peptide fragment of PTH; (b)
 CC administering the first peptide antigen to a host animal to induce
 CC antibody production; (c) monitoring the antibody titre produced; (d)
 CC isolating antisera produced in the host animal; and (e) selecting
 CC antisera from the isolated antisera produced in the host that is capable
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by
 CC the method; and (3) test kits and analytical procedures used for the
 CC determination of bioactive intact PTH utilising (ab). The methods and
 CC compositions of the present invention are useful for determining
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
 CC The antigens, antibodies and methods of the present invention, as
 CC compared to prior art, have the particular advantages of possessing
 CC greater affinity for PTH, and in particular, are designed to have a novel
 CC recognition for amino acid residues extending beyond the first N-terminal
 CC PTH residue, and further have negligible cross-reactivity with the large
 CC non-molecular forms of PTH. PTH levels are an important parameter in
 CC patients suffering from hypercalcaemia, osteoporosis and primary
 CC hyperparathyroidism. The present sequence represents a PTH antigenic
 CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,
 CC canine and bovine PTH

SO Sequence 12 AA;

Query Match 82.0%; Score 50; DB 6; Length 12;
 Best Local Similarity 90.9%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 VSEIQFMNIG 12
 2 VSEIQFMNIG 12

Db

RESULT 3

AA96968
 ID AA96968 standard; peptide; 11 AA.

XX AA96968;

DT 31-OCT-2000 (first entry)

DE Parathyroid hormone N-terminal signaling domain (residues 1-11).

XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
 KW bone remodelling; resorption; remodeling; rethert; osteoporosis.

XX Homo sapiens.

XX WO2000039278-A2.

XX 06-JUL-2000.

XX 30-DEC-1999; 99WO-US031106.

XX 31-DEC-1998; 98US-0114577P.

XX (GARD/) GARDELLA T J.

XX (KRON/) KRONENBERG H M.

XX (POTT/) POTTS J T.

(JUEP/) JUEPPNER H.

Gardella TV, Kronenberg HW, Portis JT, Jueppner H;
WPI; 2000-452384/39.

New compound comprising an amino terminal signaling functional domain
linked to a carboxy-terminal binding portion of parathyroid hormone for
treating mammalian conditions characterized by decreases in bone mass.

Claim 4; Page 92; 119pp; English.

Compounds of the structure or formula S-(L)_n-B, R₁-S-(L)_n-R or S-(L)_n-
-R, are new. S is an amino terminal signaling functional domain of
parathyroid hormone (PTH); L is a linker molecule present n times (where
n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R₁ is the
PTH-1 receptor signal sequence; and R is a portion of PTH-1 receptor
sequence. The new compounds are used for treating mammalian conditions
characterized by decreases in bone mass, determining rates of bone
reformation, bone resorption and/or bone remodeling, treating diseases
and disorders associated with decreased tether activity, increasing CAMP
in a mammalian cell having PTH-1 receptors, or screening for a peptide or
non-peptide PTH (claimed). The new compound can be administered by
inhalation unlike the large native PTH or PTHrp which avoids the need for
regular injections to treat osteoporosis

Sequence 11 AA;

Query Match 75.4%; Score 46; DB 3; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.059;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMNHL 11
: ||||| |||||
Db 1 AVSEIQLMNHL 11

RESULT 4

AAR91644
ID AAR91644 standard; peptide; 10 AA.

AC AAR91644;

DT 06-NOV-1996 (first entry)

DE Human parathyroid hormone antigenic peptide hPTH 1-10.

KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
diagnosis; active hPTH 1-37.

OS Synthetic.

PN DE4434551-A1.

PD 04-APR-1996.

PF 28-SEP-1994; 94DE-04434551.

PR 28-SEP-1994; 94DE-04434551.

PA (FORG/) FORSSMANN W.

PI Adermann K, Forssmann W, Hock D, Maegerlein M;

DR WPI; 1996-180391/19.

PT New antigenic peptide(s) from human parathyroid hormone - and antibodies
generated using them, able to distinguish between active and inactive
forms of the hormone.

PS Claim 2; Page 4; 5pp; German.

CC The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC terminal alpha-helical region and/or the non-structured region of the
CC hormone. Antibodies and their binding fragments generated by injecting an
CC animal with the peptides are useful as diagnostic reagents for
CC determination of biologically active hPTH(1-37)

Sequence 10 AA;

Query Match 73.8%; Score 45; DB 2; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMN 10
: ||||| |||||
Db 1 SVSEIQLMN 10

RESULT 5

AAV68767
ID AAV68767 standard; peptide; 10 AA.

AC AAV68767;

DT 05-MAY-2000 (first entry)

DE Amino acids 1-10 of a parathyroid hormone (PTH).

KW Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;
slimming treatment; cellulite; skin firming.

OS Unidentified.

PN W0200004047-A1.

PD 27-JAN-2000.

PF 07-JUL-1999; 99WO-FR001687.

PR 17-JUL-1998; 98FR-00009193.

PA (SEDE-) SEDERMA.

PI Lantner K;

DR WPI; 2000-171243/15.

PT New parathyroid hormone fragment peptides, used as lipolysis stimulants
in topically applied cosmetic compositions for slimming treatment of
excessive weight in hips and thighs.

PS Claim 1; Page 8; 18pp; French.

CC The present sequence represents a parathyroid hormone (PTH) fragment,
CC comprising amino acids 1-10. Parathyroid hormone fragments of the
CC invention have lipolysis stimulating activity (especially when topically
CC administered). The lipolytic activity of the peptides is enhanced when
CC they are chemically modified to increase their lipophilicity. The
CC peptides are used in cosmetic or dermatological compositions for skin
CC care. They are especially used for slimming treatment of excessive weight
CC in the thighs and hips, in the treatment of cellulite and for skin
CC firming

Sequence 10 AA;

Query Match 73.8%; Score 45; DB 3; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMN 10
: ||||| |||||
Db 1 SVSEIQLMN 10

```

RESULT 6
ID AAB86219
XX AAB86219 standard; peptide; 10 AA.
XX
XX AAB86219;
XX
XX 03-SEP-2001 (first entry)
XX
XX Human parathyroid hormone immunogenic peptide SEQ ID 1.
XX
XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
XX diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
XX hypo-parathyroidism; hyper-parathyroidism.
XX
XX Homo sapiens.
XX
XX DE19961350-A1.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99DE-01061350.
XX
XX 17-DEC-1999; 99DE-01061350.
XX
XX (IMMU-) IMMUNODIAGNOSTIK AG.
XX
XX Armbruster FP;
XX
XX WPI; 2001-376318/40.
XX
XX Determining the content of physiologically active parathyroid hormone,
XX useful in diagnosis of calcium-metabolism disorders, using two antibodies
XX reactive with different epitopes.
XX
XX Disclosure; Page 3; 10pp; German.
XX
XX This invention describes a novel method for determining (M1) the content
XX of active parathyroid hormone (A) by treating a sample with (i) antibody
XX (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
XX and including the N-terminal residue and (ii) antibody (Ab2) that
XX recognizes an epitope within the receptor-binding site of (A). The number
XX of molecules that react with both antibodies is determined and used to
XX calculate the content of physiologically active (A). The method is used
XX for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
XX hyper-parathyroidism. The method (unlike known assays) recognizes that
XX (i) some fragments of (A) shorter than the complete (84 aa) peptide are
XX active and (ii) that apparently intact peptide may be biologically
XX inactive, and also takes into account the fact that some fragments of (A)
XX are antagonistic (these have the receptor-binding site but lack the N-
XX terminus). It thus provides a true measure of the content of
XX physiologically active (A); contrast methods that measure intact peptide
XX and its 1-37 fragment which may produce falsely high values. This
XX sequence represents a peptide fragment used to illustrate the method of
XX the invention.
XX
XX Sequence 10 AA;
XX
XX Query Match 73.8%; Score 45; DB 4; Length 10;
XX Best Local Similarity 90.0%; Pred. No. 0.082;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 SVSEIQFMHN 10
XX 1 SVSEIQFMHN 10
XX
XX RESULT 7
XX ABR44166
XX ABR44166 standard; peptide; 10 AA.
XX
XX ABR44166;
XX

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XX
XX 04-AUG-2003 (first entry)
XX
XX Human parathyroid hormone (hPTH) fragment (residues 1-10).
XX
XX Fusion peptide; cat; hPTHDP; parathyroid hormone; skin; cosmetic;
XX lipolysis; human; hPTH.
XX
XX Homo sapiens.
XX
XX WO2003035697-A1.
XX
XX 01-MAY-2003.
XX
XX 06-MAY-2002; 2002WO-KR000835.
XX
XX 27-SEP-2001; 2001KR-00060245.
XX
XX 15-MAR-2002; 2002KR-00014062.
XX
XX (GLDS ) LG HOUSEHOLD & HEALTH CARE LTD.
XX
XX Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H;
XX Chang M;
XX
XX WPI; 2003-468288/44.
XX
XX Novel fusion peptide comprising self cell-penetrating Tat peptide bound
XX to human parathyroid hormone-derived peptide, useful as component of skin
XX slimming cosmetic composition.
XX
XX Claim 5; Page 6; 32pp; English.
XX
XX The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-
XX penetrating Tat peptide is bound to human parathyroid hormone-derived
XX peptide (hPTHDP). The fusion peptide is useful as a component of skin
XX slimming cosmetic composition. The fusion peptide does not cause
XX irritation, easily and safely penetrates into integument and endothelium,
XX does not cause skin disease and has superior lipolysis effects, and is
XX durable. The present sequence represents a human parathyroid hormone
XX (hPTH) fragment that can be used to construct the fusion peptide
XX
XX Sequence 10 AA;
XX
XX Query Match 73.8%; Score 45; DB 6; Length 10;
XX Best Local Similarity 90.0%; Pred. No. 0.082;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 SVSEIQFMHN 10
XX 1 SVSEIQFMHN 10
XX
XX RESULT 8
XX AAB86225
XX ID AAB86225 standard; peptide; 9 AA.
XX
XX AAB86225;
XX
XX 03-SEP-2001 (first entry)
XX
XX Human parathyroid hormone immunogenic peptide SEQ ID 7.
XX
XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
XX diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
XX hypo-parathyroidism; hyper-parathyroidism.
XX
XX Homo sapiens.
XX
XX DE19961350-A1.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99DE-01061350.
XX

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PR 17-DEC-1999; 99DE-01061350.
XX (IMMU-) IMMUNDIAGNOSTIK AG.
XX Armbruster FP;
XX WPI; 2001-376318/40.
XX
XX
XX Determining the content of physiologically active parathyroid hormone,
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT reactive with different epitopes.
XX
XX
XX Disclosure; Page 3; 10pp; German.
XX
XX This invention describes a novel method for determining (M1) the content
CC of active parathyroid hormone (A) by treating a sample with (i) antibody
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (ii) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyper-parathyroidism. The method (unlike known assays) recognizes that
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (ii) that apparently intact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention
XX
SQ Sequence 9 AA;
Query Match 67.2%; Score 41; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 VSEIQFMEN 10
DB 1 VSEIQFMEN 9
RESULT 9
AAR91645
ID AAR91645 standard; peptide; 9 AA.
XX
AC AAR91645;
XX
DT 06-NOV-1996 (first entry)
XX
DE Human parathyroid hormone antigenic peptide hPTH 1-9.
XX
KM Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
KM diagnosis; active hPTH 1-37.
XX
OS Synthetic.
XX
PN DE434551-A1.
XX
PS 04-APR-1996.
XX
PF 28-SEP-1994; 94DE-04434551.
XX
PR 28-SEP-1994; 94DE-04434551.
XX
PA (FORS/) FORSSMANN W.
XX
PI Adgermann K, Forssmann W, Hock D, Maegerlein M;
XX
DR WPI; 1996-180391/19.
XX

PT New antigenic peptide(s) from human parathyroid hormone - and antibodies
PT generated using them, able to distinguish between active and inactive
PT forms of the hormone.
XX
XX
XX Claim 2; Page 4; 5pp; German.
XX
XX The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC terminal alpha-helical region and/or the non-structured region of the
CC hormone. Antibodies and their binding fragments generated by injecting an
CC animal with the peptides are useful as diagnostic reagents for
CC determination of biologically active hPTH(1-37)
XX
SQ Sequence 9 AA;
Query Match 63.9%; Score 39; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VSEIQFMH 9
DB 1 VSEIQFMH 9
RESULT 10
AAY96981
ID AAY96981 standard; peptide; 9 AA.
XX
AC AAY96981;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain.
XX
KM PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KM bone reformation; resorption; remodeling; tetra; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Juepner H;
XX
DR WPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 11; Page 93; 119pp; English.
XX
CC Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or S-(L) n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased bone activity, increasing BMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or

CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHp which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 9 AA;

Query Match 63.9%; Score 39; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIOFMH 9
1 SVSEIOFMH 9
DB 1 SVSEIOFMH 9

RESULT 11
ID AAB86220 standard; peptide; 9 AA.

AC AAB86220;
XX
DT 03-SEP-2001 (first entry)

DE Human parathyroid hormone immunogenic peptide SEQ ID 2.

XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW diagnostic; calcium-metabolism disorder; osteopathy; antagonist;
KW hypo-parathyroidism; hyper-parathyroidism.

OS Homo sapiens.

XX DE19961350-A1.

XX PD 21-JUN-2001.

XX PF 17-DEC-1999; 99DE-01061350.

XX PR 17-DEC-1999; 99DE-01061350.

XX PA (IMMU-) IMMUNDIAGNOSTIK AG.

XX Armbruster FP;

XX WPI; 2001-376318/40.

XX Determining the content of physiologically active parathyroid hormone,
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT reactive with different epitopes.

XX Disclosure; Page 3; 10pp; German.

XX This invention describes a novel method for determining (M1) the content
CC of active parathyroid hormone (A) by treating a sample with (i) antibody
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (ii) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyper-parathyroidism. The method (unlike known assays) recognizes that
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (ii) that apparently intact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention

XX Sequence 9 AA;

Query Match 63.9%; Score 39; DB 4; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SVSEIOFMH 9
1 SVSEIOFMH 9
DB 1 SVSEIOFMH 9

RESULT 12
ID AAY50600 standard; peptide; 11 AA.

AC AAY50600;
XX
DT 09-FEB-2000 (first entry)

DE Resin bound cyclic peptide 33.

XX Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;
KW hypotensive; PTH receptor; treatment; hyper-calcaemia; hypo-calcaemia;
KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;
KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "FMOC-Ala"

FT Misc-difference 3 /note= "Ser(OctBu)"

FT Misc-difference 4 /note= "Glu(OctBu)"

FT Misc-difference 6 /note= "Gln(Trt)"

FT Misc-difference 9 /note= "His(Trt)"

FT Misc-difference 10 /note= "Asn(Trt)"

XX WO952933-A1.

XX PD 21-OCT-1999.

XX PF 15-APR-1999; 99WO-US008435.

XX PR 15-APR-1998; 96US-0081897P.

XX (RHON) RHONE-POULENC RORER PHARM INC.

XX Siedecki AW, Mancel JI;

XX WPI; 1999-633822/54.

XX Convergent synthesis of peptides for treating e.g. bone disorders.

XX Disclosure; Page 75; 85pp; English.

XX This invention describes a novel method for the preparation of peptides
CC (II) that contain both cyclic and linear peptide fragments comprising
CC sequential reaction of a resin-bound linear fragment with the cyclic
CC fragment in N-protected form and optionally other linear fragments. The
CC products of the invention have osteopathic and hypotensive activity. (II)
CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The
CC method is particularly used to prepare cyclic peptide analogs or
CC parathyroid hormone (PTH) or PTH-related peptides which are useful for
CC treating diseases that respond to treatment with agents that bind to PTH
CC receptors (with or without activation of adenyl cyclase activity), e.g.
CC hyper- or hypo-calcaemia, osteoporosis, osteopenia, hyper- or hypo-
CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also
CC for promoting repair of bone fractures. Separate synthesis of the cyclic
CC fragment allows convergent synthesis of resin-bound (II), with better
CC yields and higher throughput. The difficulties associated with
CC preparation of the bridged fragment are confined to a small peptide which

CC can be purified before reaction with the resin-bound component. AAY50568-
CC Y50614 represent the peptide fragments described in the method of the
CC invention
XX
SQ Sequence 11 AA:
Query Match 63.1%; Score 38.5; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.5;
Matches 9; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
1 SVSEIQFMNLTG 12
1 AVSEIQ-LHNLG 11
1 AVSEIQ-LHNLG 11
Db
RESULT 13
AAB01862
ID AAB01862 standard; peptide; 9 AA.
XX
AC AAB01862;
XX
DT 11-SEP-2000 (first entry)
XX
DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.
XX
KM Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KM calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
KM bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200023594-A1.
XX
PD 27-APR-2000.
XX
PF 20-OCT-1999; 99WO-US024481.
XX
PR 22-OCT-1998; 98US-0105530P.
XX
XX (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-339693/29.
XX
PT Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
XX acids that encode them, useful for treating osteoporosis.
XX
PS Disclosure; Page 26, 73pp; English.
XX
XX The invention relates to a novel parathyroid hormone (PTH) peptide
CC (AAB01859) and parathyroid hormone-related peptide (PTHrP, AAB01860), and
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC B01869). The peptides of the invention are at least 85% identical to the
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Ile or Lys; X6 is His or Ser;
CC provided that the peptide is not PTHrP(1-14). The peptides of the
CC invention also encompass fragments of peptides of the invention
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC and is necessary for the normal function of the gastrointestinal,
CC skeletal, neurological system, neuromuscular and cardiovascular systems.
CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC effect on the skeleton, and mediates calcium reabsorption, enhances
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous
CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC the renal and skeletal actions of PTH, and also bind to the PTH-1

CC receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC conditions characterized by a decrease in bone mass, such as
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC medical disorders that arise from excessive or altered action of the PTH-
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC useful in the determination of rates of bone formation, bone resorption
CC and/or bone remodeling in a patient. The peptides of the invention are
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC conventional synthetic chemistry, and can be delivered to a patient via
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC PTH-1/PTH-2 receptor agonists
XX
SQ Sequence 9 AA:
Query Match 59.0%; Score 36; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1 SVSEIQFMH 9
1 AVSEIQFMH 9
Db
RESULT 14
AAY96966
ID AAY96966 standard; peptide; 9 AA.
XX
AC AAY96966;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain (residues 1-9).
XX
XX PTH; parathyroid hormone, N-terminal; signaling domain; bone mass;
KM bone reformation; resorption; remodeling; tether; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
XX (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 4; Page 92, 119pp; English.
XX
XX Compounds of the structure or formula S-(L)-n-B, R1-S-(L)-n-R or S-(L)-n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R1 is the
CC PTH-1 receptor signal sequence; and R is a portion of PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases

CC and disorders associated with decreased lethral activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis

XX Sequence 9 AA;
SQ

Query Match 59.0%; Score 36; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9
Db 1 AVSEIQQLMH 9

RESULT 15
AAB01863
ID AAB01863 standard; peptide: 9 AA.
XX
AC AAB01863;
XX
DT 11-SEP-2000 (first entry)
XX
DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.
XX
XX Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
XX calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
XX bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200023594-A1.
XX
XX 27-APR-2000.
XX
XX 20-OCT-1999; 99WO-US024481.
XX
XX 22-OCT-1998; 98US-0105530P.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTS/) POTTS J T.
XX (JUEP/) JUEPNER H.
XX
XX Gardella TJ, Kronenberg HM, Potts JT, Juepner H;
XX WPI, 2000-339693/29.
XX
XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
XX acids that encode them, useful for treating osteoporosis.
XX
XX Disclosure: Page 26; 73pp; English.

CC The invention relates to a novel parathyroid hormone (PTH) peptide
CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC B01869). The peptides of the invention are at least 85% identical to the
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Ileu-X3-His-X4-X5-
CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC provided that the peptide is not PTHrP(1-14). The peptides of the
CC invention also encompass fragments of peptides of the invention
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC and is necessary for the normal function of the gastrointestinal,
CC skeletal, neurological system, neuromuscular and cardiovascular systems.
CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC effect on the skeleton, and mediates calcium reabsorption, enhances
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous

CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC the renal and skeletal actions of PTH, and also bind to the PTH-1
CC receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC conditions characterised by a decrease in bone mass, such as
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC medical disorders that arise from excessive or altered action of the PTH-
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC useful in the determination of rates of bone formation, bone resorption
CC and/or bone remodelling in a patient. The peptides of the invention are
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC conventional synthetic chemistry, and can be delivered to a patient via
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC PTH-1/PTH-2 receptor agonists

SQ Sequence 9 AA;
XX

Query Match 54.1%; Score 33; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9
Db 1 AVSEIQQLMH 9

Search completed: May 18, 2004, 10:01:54
Job time : 46.75 secs

Tue May 18 12:03:04 2004

us-09-730-174a-4.closed.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 10:04:51 ; Search time 33.25 Seconds
(without alignments)
100.425 Million cell updates/sec

Title: US-09-730-174A-4
Perfect score: 61
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 166097

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCF_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/PCFUS_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|------------------|
| 1 | 61 | 100.0 | 12 | US-09-730-174A-4 |
| 2 | 58 | 95.1 | 12 | US-09-730-174A-6 |
| 3 | 57 | 93.4 | 11 | US-09-730-174A-2 |
| 4 | 55 | 90.2 | 12 | US-09-730-174A-3 |
| 5 | 52 | 85.6 | 12 | US-09-730-174A-5 |
| 6 | 51 | 83.2 | 11 | US-09-730-174A-1 |
| 7 | 45 | 73.8 | 10 | US-10-168-185-1 |
| 8 | 41 | 67.2 | 9 | US-10-168-185-7 |
| 9 | 39 | 63.9 | 8 | US-10-168-185-2 |
| 10 | 37 | 60.7 | 8 | US-10-168-185-8 |
| 11 | 36 | 59.0 | 9 | US-10-192-673-6 |
| 12 | 33 | 54.1 | 9 | US-10-192-673-7 |
| 13 | 31 | 50.8 | 8 | US-10-168-185-3 |
| 14 | 29 | 47.5 | 9 | US-10-192-673-10 |
| 15 | 27 | 44.3 | 10 | US-10-033-741-61 |

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|----|----|------|----|--------------------|----------------------|
| 16 | 26 | 42.6 | 6 | US-10-168-185-5 | Sequence 5, Appl1 |
| 17 | 26 | 42.6 | 7 | US-10-168-185-4 | Sequence 4, Appl1 |
| 18 | 26 | 42.6 | 14 | US-10-192-673-8 | Sequence 8, Appl1 |
| 19 | 26 | 42.6 | 10 | US-10-168-185-11 | Sequence 11, Appl1 |
| 20 | 25 | 41.0 | 10 | US-10-137-867-526 | Sequence 2, Appl1 |
| 21 | 25 | 41.0 | 10 | US-10-366-709-2 | Sequence 45, Appl1 |
| 22 | 24 | 39.3 | 9 | US-09-834-765-45 | Sequence 65, Appl1 |
| 23 | 24 | 39.3 | 9 | US-09-834-765-55 | Sequence 73, Appl1 |
| 24 | 24 | 39.3 | 9 | US-09-834-765-73 | Sequence 78, Appl1 |
| 25 | 24 | 39.3 | 10 | US-09-834-765-78 | Sequence 8, Appl1 |
| 26 | 24 | 39.3 | 10 | US-10-233-187-8 | Sequence 14, Appl1 |
| 27 | 24 | 39.3 | 11 | US-10-153-334-14 | Sequence 16, Appl1 |
| 28 | 24 | 39.3 | 12 | US-10-319-130-16 | Sequence 508, Appl1 |
| 29 | 23 | 37.7 | 8 | US-10-043-487-508 | Sequence 26, Appl1 |
| 30 | 23 | 37.7 | 14 | US-10-147-140-26 | Sequence 120, Appl1 |
| 31 | 23 | 37.7 | 15 | US-10-024-652-120 | Sequence 339, Appl1 |
| 32 | 23 | 37.7 | 15 | US-10-024-652-339 | Sequence 407, Appl1 |
| 33 | 23 | 37.7 | 9 | US-10-024-652-407 | Sequence 956, Appl1 |
| 34 | 23 | 37.7 | 9 | US-10-024-652-1094 | Sequence 1259, Appl1 |
| 35 | 23 | 37.7 | 9 | US-10-024-652-1259 | Sequence 1464, Appl1 |
| 36 | 23 | 37.7 | 9 | US-10-024-652-1464 | Sequence 2057, Appl1 |
| 37 | 23 | 37.7 | 9 | US-10-024-652-2057 | Sequence 4, Appl1 |
| 38 | 23 | 37.7 | 10 | US-09-976-787-4 | Sequence 12, Appl1 |
| 39 | 23 | 37.7 | 10 | US-09-976-787-4 | Sequence 41, Appl1 |
| 40 | 23 | 37.7 | 10 | US-09-965-198-4 | |
| 41 | 23 | 37.7 | 10 | US-09-965-198-4 | |
| 42 | 23 | 37.7 | 10 | US-09-965-198-4 | |
| 43 | 23 | 37.7 | 10 | US-09-965-198-4 | |
| 44 | 23 | 37.7 | 10 | US-09-965-198-4 | |
| 45 | 23 | 37.7 | 10 | US-09-563-222-41 | |

ALIGNMENTS

RESULT 1
US-09-730-174A-4
Sequence 4, Appl1
Patent No. US20020110871A1
GENERAL INFORMATION:
APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Hc
FILE REFERENCE: IMUNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 4
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4

| | | |
|---|--------|---------------------------------|
| Query Match | 100.0% | Score 61, DB 9, Length 12, |
| Best Local Similarity | 100.0% | Pred No. 0/100013: |
| Matches 12; Conservative | 0; | Mismatches 0; Indels 0; Gaps 0; |
| Q1 | 1 | SVSEIQFMHNLG 12 |
| DB | 1 | SVSEIQFMHNLG 12 |
| RESULT 2 | | |
| US-09-730-174A-6 | | |
| Sequence 6, Appl1 | | |
| Patent No. US20020110871A1 | | |
| GENERAL INFORMATION: | | |
| APPLICANT: Zahradnik, R.J. | | |
| TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a | | |
| TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Hc | | |
| FILE REFERENCE: IMUNE-001A | | |

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; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-6
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Query Match      95.1%; Score 58; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.00047;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 VSEIQFMNHLG 12
Db      1 AVSEIQFMNHLG 12
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RESULT 3
US-09-730-174A-2
; Sequence 2, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-2
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Query Match      93.4%; Score 57; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      2 VSEIQFMNHLG 12
Db      1 VSEIQFMNHLG 11
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RESULT 4
US-09-730-174A-3
; Sequence 3, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3
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Query Match      90.2%; Score 55; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

Qy      1 VSEIQFMNHLG 12
Db      1 VSEIQFMNHLG 12
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RESULT 5
US-09-730-174A-5
; Sequence 5, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5
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Query Match      85.2%; Score 52; DB 9; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.0061;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 VSEIQFMNHLG 12
Db      1 AVSEIQFMNHLG 12
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```

RESULT 6
US-09-730-174A-1
; Sequence 1, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1
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```

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Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      2 VSEIQFMNHLG 12
Db      1 VSEIQFMNHLG 11
```

```

RESULT 7
US-10-168-185-1
; Sequence 1, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Mischler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
```

;; TITLE OF INVENTION: Activity in a Human Sample
;; FILE REFERENCE: HLZ-004US
;; CURRENT APPLICATION NUMBER: US/10/168,185
;; CURRENT FILING DATE: 2002-06-17
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911
;; PRIOR FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: DE 19961350
;; PRIOR FILING DATE: 1999-12-17
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-168-185-1

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQPMHN 10
Db 1 SVSEIQPMHN 10

RESULT 8
US-10-168-185-7
;; Sequence 7, Application US/10168185
;; Publication No. US20030175802A1
;; GENERAL INFORMATION:
;; APPLICANT: Armbruster, Franz Paul
;; APPLICANT: Missbichler, Albert
;; APPLICANT: Schmidt-Gayk, Heinrich
;; APPLICANT: Roth, Heinz-Jürgen
;; TITLE OF INVENTION: Method for Determining Parathormone
;; FILE REFERENCE: HLZ-004US
;; CURRENT APPLICATION NUMBER: US/10/168,185
;; CURRENT FILING DATE: 2002-06-17
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911
;; PRIOR FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: DE 19961350
;; PRIOR FILING DATE: 1999-12-17
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;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-168-185-7

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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQPMHN 10
Db 1 VSEIQPMHN 9

RESULT 9
US-10-168-185-2
;; Sequence 2, Application US/10168185
;; Publication No. US20030175802A1
;; GENERAL INFORMATION:
;; APPLICANT: Armbruster, Franz Paul
;; APPLICANT: Missbichler, Albert
;; APPLICANT: Schmidt-Gayk, Heinrich
;; APPLICANT: Roth, Heinz-Jürgen
;; TITLE OF INVENTION: Method for Determining Parathormone
;; FILE REFERENCE: HLZ-004US
;; CURRENT APPLICATION NUMBER: US/10/168,185

;; CURRENT FILING DATE: 2002-06-17
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911
;; PRIOR FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: DE 19961350
;; PRIOR FILING DATE: 1999-12-17
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-168-185-2

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Best Local Similarity 88.9%; Pred. No. 1e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQPMH 9
Db 1 SVSEIQPMH 9

RESULT 10
US-10-168-185-8
;; Sequence 8, Application US/10168185
;; Publication No. US20030175802A1
;; GENERAL INFORMATION:
;; APPLICANT: Armbruster, Franz Paul
;; APPLICANT: Missbichler, Albert
;; APPLICANT: Schmidt-Gayk, Heinrich
;; APPLICANT: Roth, Heinz-Jürgen
;; TITLE OF INVENTION: Method for Determining Parathormone
;; FILE REFERENCE: HLZ-004US
;; CURRENT APPLICATION NUMBER: US/10/168,185
;; CURRENT FILING DATE: 2002-06-17
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911
;; PRIOR FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: DE 19961350
;; PRIOR FILING DATE: 1999-12-17
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-168-185-8

Query Match 60.7%; Score 37; DB 14; Length 8;
Best Local Similarity 87.5%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SEIQPMHN 10
Db 1 SEIQPMHN 8

RESULT 11
US-10-192-673-6
;; Sequence 6, Application US/10192673
;; Publication No. US20030166838A1
;; GENERAL INFORMATION:
;; APPLICANT: Gardella, Thomas J.
;; APPLICANT: Kronenberg, Henry
;; APPLICANT: Potts, John T.
;; APPLICANT: Juppner, Harald
;; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;; FILE REFERENCE: 0609.4570002
;; CURRENT APPLICATION NUMBER: US/10/192,673
;; CURRENT FILING DATE: 2002-07-11
;; PRIOR APPLICATION NUMBER: U.S. 09/421,379

PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-192-673-6

Query Match 59.0%; Score 36; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9
DB 1 AVSEIQLMH 9

RESULT 12
US-10-192-673-7
Sequence 7, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)
FILE REFERENCE: 0609.4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-192-673-7

Query Match 54.1%; Score 33; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9
DB 1 AVSEIQLMH 9

RESULT 13
US-10-168-185-3
Sequence 3, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Misbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Rott, Heinz-Ulrich
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample

FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-185-3

Query Match 50.8%; Score 31; DB 14; Length 8;
Best Local Similarity 87.5%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 8
DB 1 SVSEIQLMH 8

RESULT 14
US-10-192-673-10
Sequence 10, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)
FILE REFERENCE: 0609.4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-192-673-10

Query Match 47.5%; Score 29; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9
DB 1 SVSEIQLMH 9

RESULT 15
US-10-033-741-61
Sequence 61, Application US/10033741
Publication No. US20030049640A1
GENERAL INFORMATION:
APPLICANT: Herman, et al.
TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Vasc
TITLE OF INVENTION: Response
FILE REFERENCE: 9195-079
CURRENT APPLICATION NUMBER: US/10/033,741

Tue May 18 12:03:04 2004

us-09-730-174a-4.closed.rapb

Page 5

;
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 61
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-741-61

Query Match 44.3%; Score 27; DB 14; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIOFMH 9
Db 1 SVSELPVH 9

Search completed: May 18, 2004, 10:20:59
Job time : 33.25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:58:45 ; Search time 12.75 Seconds
(without alignments)
48,589 Million cell updates/sec

Title: US-09-730-174A-4
Perfect score: 61
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
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5: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------------------------|
| 1 | 46 | 75.4 | 12 | 4 | US-09-442-989-31 Sequence 31, Appl |
| 2 | 45 | 73.8 | 10 | 3 | US-08-817-547A-1 Sequence 1, Appl |
| 3 | 39 | 63.9 | 9 | 3 | US-08-817-547A-2 Sequence 2, Appl |
| 4 | 36 | 59.0 | 9 | 4 | US-09-421-379-6 Sequence 6, Appl |
| 5 | 33 | 54.1 | 9 | 4 | US-09-421-379-7 Sequence 7, Appl |
| 6 | 31 | 50.8 | 8 | 3 | US-08-817-547A-3 Sequence 3, Appl |
| 7 | 29 | 47.5 | 9 | 4 | US-09-421-379-10 Sequence 10, Appl |
| 8 | 29 | 47.5 | 12 | 2 | US-08-140-137A-42 Sequence 42, Appl |
| 9 | 28 | 45.9 | 11 | 6 | 5460978-3 Patent No. 5460978 |
| 10 | 26 | 42.6 | 6 | 3 | US-08-817-547A-5 Sequence 5, Appl |
| 11 | 26 | 42.6 | 7 | 3 | US-08-817-547A-4 Sequence 4, Appl |
| 12 | 26 | 42.6 | 9 | 4 | US-09-421-379-8 Sequence 8, Appl |
| 13 | 25 | 41.0 | 12 | 2 | US-08-482-528-42 Sequence 42, Appl |
| 14 | 25 | 41.0 | 12 | 2 | US-08-482-528-42 Sequence 42, Appl |
| 15 | 24 | 39.3 | 5 | 2 | US-08-177-109A-56 Sequence 56, Appl |
| 16 | 24 | 39.3 | 5 | 2 | US-08-667-706-56 Sequence 56, Appl |
| 17 | 24 | 39.3 | 5 | 3 | US-08-817-547A-17 Sequence 17, Appl |
| 18 | 24 | 39.3 | 6 | 3 | US-08-817-547A-16 Sequence 16, Appl |
| 19 | 24 | 39.3 | 7 | 3 | US-08-817-547A-15 Sequence 15, Appl |
| 20 | 24 | 39.3 | 8 | 2 | US-08-748-021-64 Sequence 64, Appl |
| 21 | 24 | 39.3 | 8 | 3 | US-08-817-547A-14 Sequence 14, Appl |
| 22 | 24 | 39.3 | 8 | 3 | US-08-817-547A-13 Sequence 13, Appl |
| 23 | 24 | 39.3 | 9 | 3 | US-08-817-547A-7 Sequence 7, Appl |
| 24 | 24 | 39.3 | 10 | 3 | US-08-817-547A-7 Sequence 7, Appl |
| 25 | 23 | 37.7 | 9 | 1 | US-07-822-043-26 Sequence 26, Appl |
| 26 | 23 | 37.7 | 9 | 1 | US-08-346-455B-26 Sequence 26, Appl |
| 27 | 23 | 37.7 | 9 | 3 | US-08-977-221-26 Sequence 26, Appl |

| | | | | | |
|----|----|------|----|---|---------------------------------------|
| 28 | 23 | 37.7 | 9 | 4 | US-09-483-631B-26 Sequence 26, Appl |
| 29 | 23 | 37.7 | 9 | 5 | PCT-US95-06613-26 Sequence 26, Appl |
| 30 | 23 | 37.7 | 10 | 2 | US-08-116-778B-9 Sequence 9, Appl |
| 31 | 23 | 37.7 | 10 | 2 | US-08-438-562-9 Sequence 9, Appl |
| 32 | 23 | 37.7 | 10 | 2 | US-08-483-528B-97 Sequence 97, Appl |
| 33 | 23 | 37.7 | 10 | 3 | US-08-783-853A-12 Sequence 12, Appl |
| 34 | 23 | 37.7 | 10 | 3 | US-08-836-561-49 Sequence 49, Appl |
| 35 | 23 | 37.7 | 10 | 3 | US-09-280-028-12 Sequence 12, Appl |
| 36 | 23 | 37.7 | 10 | 4 | US-09-344-050-12 Sequence 12, Appl |
| 37 | 23 | 37.7 | 10 | 4 | US-09-393-385B-108 Sequence 108, Appl |
| 38 | 23 | 37.7 | 10 | 4 | US-09-434-122-49 Sequence 49, Appl |
| 39 | 23 | 37.7 | 10 | 4 | US-09-091-071-3 Sequence 3, Appl |
| 40 | 23 | 37.7 | 11 | 4 | US-09-556-605-61 Sequence 61, Appl |
| 41 | 23 | 37.7 | 12 | 3 | US-09-064-750-1 Sequence 1, Appl |
| 42 | 23 | 37.7 | 12 | 4 | US-09-556-605-60 Sequence 60, Appl |
| 43 | 22 | 36.1 | 10 | 1 | US-08-615-181-83 Sequence 83, Appl |
| 44 | 22 | 36.1 | 10 | 1 | US-08-555-579-2 Sequence 2, Appl |
| 45 | 22 | 36.1 | 10 | 2 | US-08-428-257A-14 Sequence 14, Appl |

ALIGNMENTS

RESULT 1
US-09-442-989-31
Sequence 31, Application US/09442989
Parent No. 6569993
GENERAL INFORMATION:
APPLICANT: Sledeski, Adam W.
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
FILE REFERENCE: A3113B-US
CURRENT FILING DATE: 1999-11-18
EARLIER APPLICATION NUMBER: 60/081,897
EARLIER FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 12
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)
OTHER INFORMATION: FMOC-Ala
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (3)
OTHER INFORMATION: Ser(OCBu)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (4)
OTHER INFORMATION: Glu(OCBu)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (6)
OTHER INFORMATION: Glu(Trt)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (9)
OTHER INFORMATION: His(Trt)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (10)
OTHER INFORMATION: Asn(Trt)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: N1e
US-09-442-989-31

Tue May 18 12:03:03 2004

us-09-730-174a-4.closed.ra1

Page 2

Query Match 75.4%; Score 46; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CY 1 SVSEIOFMHNG 12
1 AVSEIOQLXHNLS 12
DB

RESULT 2
US-08-817-547A-1
Sequence 1, Application US/08817547A
Patent No. 6030790
GENERAL INFORMATION:
APPLICANT: Ademann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-817-547A-1

Query Match 73.8%; Score 45; DB 3; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 SVSEIOFMHNG 10
1 SVSEIOQLXHNLS 10
DB

RESULT 3
US-08-817-547A-2
Sequence 2, Application US/08817547A
Patent No. 6030790
GENERAL INFORMATION:
APPLICANT: Ademann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence

NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-817-547A-2

Query Match 63.9%; Score 39; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e-05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 SVSEIOFMHNG 9
1 SVSEIOQLXHNLS 9
DB

RESULT 4
US-09-421-379-6
Sequence 6, Application US/09421379
Patent No. 6495662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
FILE REFERENCE: 0609.4570001
CURRENT APPLICATION NUMBER: US/09/421,379
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 6
LENGTH: 9
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-6

Tue May 18 12:03:03 2004

us-09-730-174a-4.closed.rai

Page 3

Query Match 59.0%; Score 36; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 SVSEIQFMH 9
DB 1 AVSEIQQLMH 9

RESULT 5
US-09-421-379-7
Sequence 7, Application US/09421379
Patent No. 6495662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
FILE REFERENCE: 0609.4570001
CURRENT APPLICATION NUMBER: US/09/421,379
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-7

Query Match 54.1%; Score 33; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SVSEIQFMH 9
DB 1 AVSEIQQLMH 9

RESULT 6
US-08-817-547A-3
Sequence 3, Application US/08817547A
Patent No. 6030790
GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-817-547A-3

Query Match 50.8%; Score 31; DB 3; Length 8;
Best Local Similarity 87.5%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SVSEIQFMH 8
DB 1 SVSEIQQLM 8

RESULT 7
US-09-421-378-10
Sequence 10, Application US/09421379
Patent No. 6495662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
FILE REFERENCE: 0609.4570001
CURRENT APPLICATION NUMBER: US/09/421,379
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-378-10

Query Match 47.5%; Score 29; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SVSEIQFMH 9
DB 1 SVSEHQQLH 9

RESULT 8
US-08-140-137A-42
Sequence 42, Application US/08140137A
Patent No. 5817617
GENERAL INFORMATION:
APPLICANT: TUOMANEN, ELAINE
APPLICANT: MASURE, H. R.

Tue May 18 12:03:03 2004

us-09-730-174a-4.closed.ra1

Page 4

TITLE OF INVENTION: ANALOGS OF ENDOTHELIAL LEUCOCYTE
TITLE OF INVENTION: ADHESION MOLECULE (ELAM)
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klaubner & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/140,137A
FILING DATE: 27-MAY-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-096
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: Card peptide sequence
US-08-140-137A-42

Query Match 47.5%; Score 29; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSEIQFMH 9
: || || || ||
Db 5 ISEBQFVH 12

RESULT 9
5460978-3
Patent No. 5460978
APPLICANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,
BRUCE E.; WETTENHALL, RICHARD E.H.
TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL
HYPERCALCEMIA OF MALIGNANCY-PTHRP
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/715,280
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 199,235
FILING DATE: 09-MAY-1988
APPLICATION NUMBER:
FILING DATE:
SEQ ID NO: 3:
LENGTH: 11
5460978-3

Query Match 45.9%; Score 28; DB 6; Length 11;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 10
: || || || || ||
Db 1 AVSEHOLEHN 10

RESULT 10
US-08-817-547A-5
Sequence 5, Application US/08817547A
Patent No. 6030790
GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: no
ANTI-SENSE: no
US-08-817-547A-5

Query Match 42.6%; Score 26; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQ 6
: || || || || ||
Db 1 SVSEIQ 6

RESULT 11
US-08-817-547A-4
Sequence 4, Application US/08817547A
Patent No. 6030790
GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-817-547A-4

Query Match 42.6%; Score 26; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIO 6
DB 1 SVSEIO 6

RESULT 12
US-09-421-379-8
Sequence 8, Application US/09421379
Patent No. 6485662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)
FILE REFERENCE: 0609.4570001
CURRENT APPLICATION NUMBER: US/09/421,379
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-8

Query Match 42.6%; Score 26; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 3e+05;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIOFMH 9
DB 1 AVSEHQLH 9

RESULT 13
US-08-482-228-42
Sequence 42, Application US/08482228
Patent No. 5968753
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy L.
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,228
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-228-42

Query Match 41.0%; Score 25; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SEIOFMH 9
DB 5 SSVTFMH 11

RESULT 14
US-08-482-528-42
Sequence 42, Application US/08482528
Patent No. 6017719
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy L.
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210

CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,528
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gutheirie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ. ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-528-42

Query Match 41.0%; Score 25; DB 3; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SEIQPMH 9
DB 5 SSVTFMH 11

RESULT 15
US-08-177-109A-56
Sequence 56, Application US/08177109A
Patent No. 5868615
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/177,109A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ. ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-08-177-109A-56

Query Match 39.3%; Score 24; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MENLG 12
DB 1 LHMNG 5

Search completed: May 18, 2004, 10:06:44
Job time : 13.75 secs

Tue May 18 12:03:08 2004

us-09-730-174a-5.closed.rpr

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:56:10 ; Search time 10.25 seconds
(without alignments)
112.614 Million cell updates/sec

Title: US-09-730-174A-5
Perfect score: 59
Sequence: 1 AVSEIQLMNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1591

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------|
| 1 | 21 | 35.6 | 12 | 2 | S21205 Ig heavy chain V r |
| 2 | 18 | 30.5 | 7 | 2 | A58718 carnocin U149 - Ca |
| 3 | 18 | 30.5 | 9 | 2 | S78420 ribosomal protein |
| 4 | 18 | 30.5 | 10 | 2 | A60589 sperm-activating p |
| 5 | 18 | 30.5 | 10 | 2 | B46453 e antigen p20e pre |
| 6 | 18 | 30.5 | 12 | 2 | A55837 5-aminimidazole r |
| 7 | 17 | 28.8 | 7 | 2 | 146868 alpha-myosin heavy |
| 8 | 17 | 28.8 | 10 | 2 | A37268 T-cell receptor al |
| 9 | 17 | 28.8 | 12 | 2 | PH1190 T-cell receptor al |
| 10 | 17 | 28.8 | 12 | 2 | PH1187 T-cell receptor al |
| 11 | 17 | 28.8 | 12 | 2 | PH1189 placental lactogen |
| 12 | 16 | 27.1 | 10 | 2 | A47364 T-cell receptor be |
| 13 | 16 | 27.1 | 11 | 2 | PH0924 p1f protein - Bac |
| 14 | 15 | 25.4 | 7 | 2 | S25266 polyphosphate-gluc |
| 15 | 15 | 25.4 | 7 | 2 | S29735 chlorophyll a/b-bi |
| 16 | 15 | 25.4 | 9 | 2 | PM0002 N-methylpurine DNA |
| 17 | 15 | 25.4 | 9 | 2 | A56029 T-cell receptor ga |
| 18 | 15 | 25.4 | 10 | 2 | A49033 rhodopsin homolog |
| 19 | 15 | 25.4 | 11 | 2 | A38841 transactin elonga |
| 20 | 15 | 25.4 | 11 | 2 | B41835 glycoprotein H-a - |
| 21 | 15 | 25.4 | 11 | 2 | A40795 COI intron 16 prot |
| 22 | 14 | 23.7 | 4 | 2 | I38888 NADH2 dehydrogenas |
| 23 | 14 | 23.7 | 7 | 2 | T09512 Ig heavy chain CRD |
| 24 | 14 | 23.7 | 9 | 2 | PT0238 neuromedin K - pig |
| 25 | 14 | 23.7 | 10 | 1 | SPGNK cytochrome b559 co |
| 26 | 14 | 23.7 | 10 | 2 | S28055 hypothetical prote |
| 27 | 14 | 23.7 | 10 | 2 | S27873 ranatichykinin C - |
| 28 | 14 | 23.7 | 10 | 2 | C61033 amine oxidase (cop |
| 29 | 14 | 23.7 | 11 | 2 | S71304 |

| | | | | | |
|----|----|------|----|---|--------|
| 30 | 14 | 23.7 | 11 | 2 | S60354 |
| 31 | 14 | 23.7 | 11 | 2 | B29806 |
| 32 | 14 | 23.7 | 11 | 4 | S41909 |
| 33 | 14 | 23.7 | 12 | 2 | S25485 |
| 34 | 14 | 23.7 | 12 | 2 | G49410 |
| 35 | 14 | 23.7 | 12 | 2 | S71034 |
| 36 | 14 | 23.7 | 12 | 2 | PH1175 |
| 37 | 14 | 23.7 | 12 | 2 | PH1174 |
| 38 | 14 | 23.7 | 12 | 2 | I41235 |
| 39 | 13 | 22.0 | 6 | 2 | PQ0008 |
| 40 | 13 | 22.0 | 8 | 2 | T14906 |
| 41 | 13 | 22.0 | 8 | 2 | TS0316 |
| 42 | 13 | 22.0 | 8 | 2 | PH1618 |
| 43 | 13 | 22.0 | 9 | 2 | S13636 |
| 44 | 13 | 22.0 | 9 | 2 | UN0026 |
| 45 | 13 | 22.0 | 9 | 2 | PT0231 |

ALIGNMENTS

RESULT 1
S21205
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C:Accession: S21205
R:Makiya, R., Stigbrand, T.
Eur. J. Biochem. 205, 341-345, 1992
A:Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin
A:Reference number: S21205; PMID:92209522; PMID:1555592
A:Accession: S21205
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <NA>
C:Keywords: heterotrimer; immunoglobulin

Query Match 35.6%; Score 21; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 6.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 EIQMLNLG 12
Db 1 EVQIVESGG 9

RESULT 2
A58718
carnocin U149 - Carnobacterium sp. (fragment)
C:Species: Carnobacterium sp.
C>Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
R:Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Hojo, H.; Nes, I.F.
Appl. Environ. Microbiol. 58, 1417-1422, 1992
A:Title: Purification and characterization of a new bacteriocin isolated from a Carnobac
A:Reference number: A58718; PMID:92321768; PMID:1622206
A:Accession: A58718
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <STO>
C:Keywords: antibiotic; lanthionine

Query Match 30.5%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6
Db 2 SEIQ 5

RESULT 3
S78420

ribosomal protein RL41, mitochondrial [validated] - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #ext_change 21-Jul-2000

C/Accession: S78420

R/Soldschmidt-Reisin, S.; Graack, H.R.

A/Reference number: S78411

A/Accession: S78420

A/Molecule type: protein

A/Residues: 1-9 <GOL>

A/Note: the protein is designated as mitochondrial ribosomal protein L41

C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match

Best Local Similarity 30.5%; Score 18; DB 2; Length 9;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12

DB 5 HRLG 8

RESULT 4

A60589

specm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchi

C/Species: Heterocentrotus mammillatus

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #ext_change 18-Aug-2000

C/Accession: A60589

R/Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi, K.

A/Title: A halogenated amino acid-containing sperm activating peptide and its related pe

ptide andus; Echinosmetra machaei and Heterocentrotus mammillatus.

A/Reference number: A60527

A/Accession: A60589

A/Molecule type: protein

A/Residues: 1-10 <YOS>

C/Superfamily: unassigned animal peptides

Query Match

Best Local Similarity 30.5%; Score 18; DB 2; Length 10;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNLG 12

DB 2 YNLG 5

RESULT 5

B46453

e antigen p20e precursor - hepatitis B virus (subtype adr) (fragment)

N/Alternate names: HBe antigen precursor

C/Species: hepatitis B virus, HBV

A/Variety: subtype adr

C/Date: 18-Jun-1993 #sequence_revision 08-Nov-1996 #ext_change 15-Aug-1997

C/Accession: B46453

R/Takahashi, K.; Kishimoto, S.; Ohori, K.; Yoshizawa, H.; Machida, A.; Ohnuma, H.; Tsuda

J. Immunol. 147, 3156-3160, 1991

A/Title: Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepa

A/Reference number: A46453; PMID:9201314; PMID:1717588

A/Accession: B46453

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <TAK>

A/Experimental source: subtype adr

A/Note: sequence extracted from NCBI backbone (NCBI:60243)

F:1-10/Domain: signal sequence (fragment) #status predicted <SIG>

Query Match

Best Local Similarity 30.5%; Score 18; DB 2; Length 10;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 IOLMH 9

DB 1 MOLFH 5

RESULT 6

A55837

5-aminimidazole ribonucleotide carboxylase/4-N-succinylamino carbonyl-5-aminimidazole

C/Species: Gallus gallus (chicken)

C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #ext_change 17-Mar-1999

C/Accession: A55837

R/Firestone, S.M.; Davison, V.J.

A/Title: Carboxylases in de Novo purine biosynthesis. Characterization of the Gallus gal

A/Reference number: A55837; PMID:95001903; PMID:7918410

A/Accession: A55837

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-12 <FIR>

Query Match

Best Local Similarity 30.5%; Score 18; DB 2; Length 12;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVEFIOL 7

DB 2 AAEIOL 8

RESULT 7

146868

alpha-myosin heavy chain - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #ext_change 05-Nov-1999

C/Accession: 146868

R/Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.

A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula

A/Reference number: 146868; PMID:84221901; PMID:6328491

A/Accession: 146868

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-7 <PRI>

A/Cross-references: GB:X01698; NID:g165538; PIDN:AAA1415.1; PID:g165539

Query Match

Best Local Similarity 28.8%; Score 17; DB 2; Length 7;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QLMHN 10

DB 1 QXKMD 5

RESULT 8

A37268

1g heavy chain C region (129) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #ext_change 13-Mar-1998

C/Accession: A37268

R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

A/Title: Heavy and light chain variable region sequences and antibody properties of anti

A/Reference number: A37440; PMID:91177923; PMID:1106720

A/Accession: A37268

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-10 <RUF>

Query Match

Best Local Similarity 28.8%; Score 17; DB 2; Length 10;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQLMHNLG 12

Db 1 ESQSFNNVG 9

RESULT 9

PH1190
T-cell receptor alpha chain V region (CW3/10.1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1190
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytoolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: PH1190
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>

Query Match 28.8%; Score 17; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSE 4
|||
Db 2 AVSE 5

RESULT 10

PH1187
T-cell receptor alpha chain V region (CW3/1F11) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1187
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytoolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: PH1187
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>

Query Match 28.8%; Score 17; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSE 4
|||
Db 2 AVSE 5

RESULT 11

PH1189
T-cell receptor alpha chain V region (CW3/2C3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1189
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytoolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: PH1189
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>

Query Match 28.8%; Score 17; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSE 4
|||

Db 2 AVSE 5

RESULT 12

A47364
Placental lactogen-I precursor - mouse (fragment)
C/Species: Mus sp. (mouse)
C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C/Accession: A47364
R/Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.
Mol. Endocrinol. 7, 181-188, 1993
A/Title: Trophoblast-specific transcription from the mouse placental lactogen-I gene pro
A/Reference number: A47364; MUID:9225959; PMID:8469232
A/Accession: A47364
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-10 <RES>
A/Cross-references: GB:S58124; MUID:9299449

Query Match 27.1%; Score 16; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IOLMNL 11
|||
Db 1 MOLTNL 7

RESULT 13

PH0924
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C/Accession: PH0924
R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A/Reference number: PH0924; MUID:92078857; PMID:1836012
A/Accession: PH0924
A/Molecule type: mRNA
A/Residues: 1-11 <GOL>
A/Experimental source: concanavalin A-activated lymphoblast
C/Keywords: T-cell receptor

Query Match 27.1%; Score 16; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIOLM 8
|||
Db 2 ASSGMDLM 9

RESULT 14

S25266
pIIE protein - Escherichia coli (fragment)
C/Species: Escherichia coli
C/Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 11-Jun-1993
C/Accession: S25266
R/Dunay, B.; Taha, M.K.; Poser, O.; Marchal, C.; Pugsley, A.P.
Mol. Microbiol. 6, 1887-1894, 1992
A/Title: pIIE, a component of the pullulanase secretion pathway of Klebsiella oxytoca,
A/Reference number: S25266; MUID:92374839; PMID:1354833
A/Accession: S25266
A/Molecule type: protein
A/Residues: 1-7 <DUP>
C/Genetics:
A/Gene: pIIE

Query Match 25.4%; Score 15; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IOM 8
|:|
Db 4 IELM 7

RESULT 15

S29735
polyphosphate-glucose phosphotransferase (EC 2.7.1.63) - *Propionibacterium freudenreichii*
C;Species: *Propionibacterium freudenreichii* subsp. *shermanii*
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
C;Accession: S29735
R;Phillips, N.F.B.; Horn, P.J.; Wood, H.G.
Arch. Biochem. Biophys. 300, 309-319, 1993
A;Title: The polyphosphate- and ATP-dependent glucokinase from *Propionibacterium shermanii*
A;Reference number: S29735; PMID:93143332; PMID:8380966
A;Accession: S29735
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <PH1>
C;Keywords: phosphotransferase

Query Match 25.4%; Score 15; DB 2; length 7;
Best Local Similarity 75.0%; Pred.No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12
|:|
Db 2 HVLG 5

Search completed: May 18, 2004, 10:05:41
Job time : 11.25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:43:45 ; Search time 6.75 Seconds
(without alignments)

92.569 Million cell updates/sec

Title: US-09-730-174A-5
Sequence: 1 AVSEIQMLNMLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141661 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | # Query Match | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|-------------|
| 1 | 18 | 30.5 | 7 | 1 | LANC_CARUT |
| 2 | 16 | 27.1 | 8 | 1 | ALB6_CYPDO |
| 3 | 16 | 27.1 | 8 | 1 | FUS5_FUSO |
| 4 | 16 | 27.1 | 11 | 1 | EBG_CLOPA |
| 5 | 15 | 25.4 | 11 | 1 | PKV1_PRRAM |
| 6 | 15 | 23.7 | 6 | 1 | TRP1_PSPPU |
| 7 | 14 | 23.7 | 7 | 1 | AL17_CYPDO |
| 8 | 14 | 23.7 | 8 | 1 | AL13_CARMA |
| 9 | 14 | 23.7 | 8 | 1 | AL11_CYPDO |
| 10 | 14 | 23.7 | 9 | 1 | FAR8_MACRS |
| 11 | 14 | 23.7 | 9 | 1 | UF02_MOUSE |
| 12 | 14 | 23.7 | 10 | 1 | AL19_CARMA |
| 13 | 14 | 23.7 | 10 | 1 | PSBF_CAPAN |
| 14 | 14 | 23.7 | 10 | 1 | TEMK_PANTE |
| 15 | 14 | 23.7 | 10 | 1 | TKNC_RANCA |
| 16 | 14 | 23.7 | 10 | 1 | TKNK_PTC |
| 17 | 14 | 23.7 | 11 | 1 | ASL1_BACSE |
| 18 | 14 | 23.7 | 12 | 1 | CD11_LITXA |
| 19 | 14 | 23.7 | 12 | 1 | CD14_LITXA |
| 20 | 14 | 23.7 | 12 | 1 | POPD_MERTM |
| 21 | 14 | 23.7 | 12 | 1 | RS19_TOBRP |
| 22 | 14 | 22.0 | 8 | 1 | LCK4_LEBMA |
| 23 | 13 | 22.0 | 8 | 1 | LCK6_LEBMA |
| 24 | 13 | 22.0 | 9 | 1 | MOSH_CLYXA |
| 25 | 13 | 22.0 | 9 | 1 | PPK1_PRRAM |
| 26 | 13 | 22.0 | 10 | 1 | RRPL_PRRAM |
| 27 | 13 | 22.0 | 11 | 1 | CSIS_BACSU |
| 28 | 13 | 22.0 | 11 | 1 | O2QA_COMTE |
| 29 | 13 | 22.0 | 12 | 1 | PKK4_PRRAM |
| 30 | 13 | 20.3 | 9 | 1 | FIB3_PAPHA |
| 31 | 12 | 20.3 | 9 | 1 | RE42_LITRU |
| 32 | 12 | 20.3 | 10 | 1 | GLEM_HUMAN |
| 33 | 12 | 20.3 | 10 | 1 | GONI_CLOPA |

| | | | | | |
|----|----|------|----|---|------------|
| 34 | 12 | 20.3 | 10 | 1 | GON2_CHEPR |
| 35 | 12 | 20.3 | 10 | 1 | HTR1_ROMMI |
| 36 | 12 | 20.3 | 10 | 1 | HTE_HELZE |
| 37 | 12 | 20.3 | 10 | 1 | SVK_CAMUP |
| 38 | 12 | 20.3 | 10 | 1 | TKNB_RANR1 |
| 39 | 12 | 20.3 | 11 | 1 | CX11_CONMR |
| 40 | 12 | 20.3 | 11 | 1 | HS70_PINPS |
| 41 | 12 | 20.3 | 11 | 1 | T2P1_PRRAM |
| 42 | 12 | 20.3 | 12 | 1 | HEP1_BACSE |
| 43 | 12 | 20.3 | 12 | 1 | PPK4_PRRAM |
| 44 | 11 | 18.6 | 7 | 1 | TY51_LITRU |
| 45 | 11 | 18.6 | 7 | 1 | UN06_PINPS |

ALIGNMENTS

RESULT 1
LANC_CARUT STANDARD; PRT; 7 AA.
AC P36560; 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin U149 (Fragment).
OS Carnobacterium sp. (strain U149).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
CC Carnobacterium.
OK NCBI_TaxID=35782;
RN [1]
RP MEDLINE=92321768; Pubmed=1622206;
RX Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
Nes I.F.;
RA "Purification and characterization of a new bacteriocin isolated from
a Carnobacterium sp.";
RT Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -1- FUNCTION: Lantibiotin-containing peptide antibiotic (lantibiotic).
KW Active on Gram-positive bacteria.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON TER
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 30.5%; Score 18; DB 1; Length 7;
Best local similarity 100.0%; Pred. No. 1.4e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6
DB 2 SEIQ 5

RESULT 2
ALB6_CYPDO STANDARD; PRT; 8 AA.
AC P82157; 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OK NCBI_TaxID=82600;

SEQUENCE.
TISSE=Latva; PubMed=9392829;
MEDLINE=98054539; Pubmed=9392829;
Duke H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,
Davy M., East P.D., Thorpe A.;
RA "Lepidopteran peptides of the allatostatin superfamily.";
RT Peptides 18:1301-1309(1997).

CC -1- SIMILARITY: Belongs to the allostatin family.
KM Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 27.1%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MHNLG 12
Db 3 LVNFG 7

RESULT 3
FUSS_FUSSO STANDARD; PRT; 8 AA.
ID FUSS_FUSSO
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Allergen Fus s 13596* (Fragment).
DE Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J.; Gangal S.V.;
RL Submitted (JUL-1997) to Swiss-Prot.
CC -1- ALLERGEN: Causes an allergic reaction in human.
KW Allergen.
FT NON TER
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B65041 CRC64;

Query Match 27.1%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMHNL 11
Db 3 MSHNV 7

RESULT 4
ERG_CLOPA STANDARD; PRT; 11 AA.
ID ERG_CLOPA
AC P81501;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=MS;
RA MEDLINE=98291870; PubMed=9629918;
RX Flengsund R.; Skjeldal L.;
RT "Two-dimensional gel electrophoresis, separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of
the nascent protein chain from the A-site to the P-site of the
ribosome.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro; IP000795; EF_GTPbind.

DR PROSITE; PS00301; EFACOR_GTP; PARTIAL.
KM Elongation factor; Protein biosynthesis; GTP-binding.
FT NON TER 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 27.1%; Score 16; DB 1; Length 11;
Best Local Similarity 25.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 IQLMHNLG 12
Db 4 LEKFNIG 11

RESULT 5
PVKL_PERAM STANDARD; PRT; 11 AA.
ID PVKL_PERAM
AC P41837;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-1 (Pea-PVK-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Abdominal periviscerokinin organs;
RA MEDLINE=95232021; PubMed=7716075;
RX Predel R.; Linde D.; Rapus J.; Vettermann S.; Penzlin H.;
RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
periviscerokinin organs of the American cockroach.";
RL Peptides 16:61-66(1995).
CC -1- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
HYPERNEURAL MUSCLE.
KW Neuropeptide; Amidation.
FT MOD RES 11
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 25.4%; Score 15; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IQLMHN 10
Db 6 IPVMRN 11

RESULT 6
TRPI_PSEPU STANDARD; PRT; 6 AA.
ID TRPI_PSEPU
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE HTH-type transcriptional regulator trpi (TrpBA operon transcriptional
activator) (Fragment).
GN TRPI.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PPG1 C18;
RX MEDLINE=89335826; PubMed=2503057;
RA Eberly L.; Crawford I.P.;
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
putida.";
RL Biochimie 71:521-531(1999).
CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING

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CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRP1 BINDS UPSTREAM OF THE
CC TRAP OPERON OVERLAPPING ITS OWN PROMOTER REGION.
CC -1- SIMILARITY: Contains 1 HTH lyase-type DNA-binding domain.
CC -----
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CC -----
CC EMBL: X13299; CAA31660.1; -.
CC InterPro: IPR000847; HTH_LYER.
CC PROSITE: PS50911; HTH_LYER; PARTIAL.
CC Trypophan biosynthesis; Transcription regulation; Activator;
CC DNA binding.
CC MOD RES 6 6
CC NON_TER
CC SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
CC -----
Query Match 23.7%; Score 14; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 7 LHMNL 11
Db 1 MANDL 5

RESULT 7
ALL7_CYDPO STANDARD; PRT; 7 AA.
ID ALL7_CYDPO
AC P82158;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastratin 7.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OC NCBI_Taxid=82600;
OX NCBI_Taxid=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Davey H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
CC KW Neuropeptide; Amidation.
CC MOD RES 7
CC FT SEQUENCE 7 AA; 873 MW; 672879CAB8569350 CRC64;
CC -----
Query Match 23.7%; Score 14; DB 1; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 8 MNLG 12
Db 2 MYDFG 6

RESULT 8
AL18_CARMA STANDARD; PRT; 8 AA.
ID AL18_CARMA
AC P81821;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 18.

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OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_Taxid=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Davey H., Johnsen A.H., Maestro J.-L., Scott A.G., Jares P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Bur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -1- SIMILARITY: Belongs to the allatostatin family.
CC KW Neuropeptide; Amidation; Multigene family.
CC MOD RES 8
CC FT SEQUENCE 8 AA; 919 MW; C82879D5AB5692A5 CRC64;
CC -----
Query Match 23.7%; Score 14; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 8 MNLG 12
Db 3 MYDFG 7

RESULT 9
ALL1_CYDPO STANDARD; PRT; 8 AA.
ID ALL1_CYDPO
AC P82152;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastratin 1.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OC NCBI_Taxid=82600;
OX NCBI_Taxid=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Davey H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
CC KW Neuropeptide; Amidation.
CC MOD RES 8
CC FT SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;
CC -----
Query Match 23.7%; Score 14; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 9 HNLG 12
Db 4 YNFG 7

RESULT 10
FAR8_MACRS STANDARD; PRT; 9 AA.
ID FAR8_MACRS
AC P83281;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLR8 (VSHNRLRF-amide).
DE Macrobrachium rosenbergii (Giant fresh water prawn).

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OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxId=79674;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=1179812;
RA Sithigorngul P., Sarathongskum W., Longyant S., Panchan N.,
RA Sithigorngul W., Petsom A.;
RT "Three more novel FMRFamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:151-157(2001).
CC -1- SIMILARITY: Belongs to the FAPR (FMRFamide related peptide)
CC family.
CC GO: GO:0007218; P:neuropeptide signaling pathway; IDA.
KM Neuropeptide; Amidation.
FT MOD_RSS 9
SQ SEQUENCE 9 AA; 1133 MW; 845A0729C44441F5 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HN 10
DB 3 HN 4

RESULT 11
UF02_MOUSE STANDARD; PRT; 9 AA.
AC P38640;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.0, its MW is: 32 kDa.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1102 MW; 7E73EA36D05B1AAB CRC64;

Query Match 23.7%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIQ 6
DB 4 EIQ 6

RESULT 12
AL19_CARMA STANDARD; PRT; 10 AA.
AC PA1822;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinstatin 19.
OS Carcinus maenas (Common shore crab) (Green crab).

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OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxId=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Dure H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thore A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -1- SIMILARITY: Belongs to the allatostatin family.
KM Neuropeptide; Amidation; Multigene family.
FT MOD_RSS 10
SQ SEQUENCE 10 AA; 1101 MW; 96687CD5A563A81 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MNING 12
DB 5 MYSFG 9

RESULT 13
PSBF_CAPAN STANDARD; PRT; 10 AA.
AC Q03367;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b559 beta subunit (PSII reaction center subunit VII)
DE (Fragment).
OS Capsicum annuum (Bell pepper).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxId=4072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;
RX MEDLINE=9309270; PubMed=1463853;
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;
RT "The publ gene from bell pepper (Capsicum annuum): plastid RNA
RT editing also occurs in non-photosynthetic chromoplasts.";
RL Plant Mol. Biol. 20:1185-1188(1992).
CC -1- FUNCTION: This D-type cytochrome is tightly associated with the
CC reaction center of photosystem II and possibly is part of the
CC water-oxidation complex.
CC -1- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC -1- SIMILARITY: Belongs to the psbE / psbF family.
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CC EMBL: X65570; CAA46539.1; -
CC FIR; S28055; S28055.
CC HAMAP: MF_00643; -; 1.
CC InterPro: IPR006216; Cyt_b559.
CC PROSITE: PS00537; CYTOCHROME_B559; PARTIAL.
CC Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT NON_TER 1

```

FT TRANSMEM <1 5 BY SIMILARITY.
 FT DOMAIN 6 10 LUMENAL (POTENTIAL).
 SQ SEQUENCE 10 AA; 1180 MW; 817D0F59D6D6DC5 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;
 Best Local Similarity 25.0%; Pred. No. 7.7e+03;
 Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVEFQQLM 8
 DB 1 SISAMQFI 8

RESULT 14
 TEMK_RANCA STANDARD; PRT; 10 AA.
 ID TEMK_RANCA
 AC P56923;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Temporin K.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OC NCBI_Taxid=8407;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simaco M., Magnogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Bara D.;
 RA "Temporins, antimicrobial peptides from the European red frog Rana
 RT temporaria";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -1- FUNCTION: Has antibacterial activity against Gram-positive
 CC bacteria.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- SIMILARITY: Belongs to the brevinin family.
 KM Amphibian defense peptide; Antibiotic; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LHMNL 11
 DB 1 LLEPL 5

RESULT 15
 TKNC_RANCA STANDARD; PRT; 10 AA.
 ID TKNC_RANCA
 AC P22690;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranachykinin C (RTK C).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OC NCBI_Taxid=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Intestine;
 RX MEDLINE=91254337; PubMed=2041143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT Isolation of four novel tachykinins from frog (Rana catesbeiana)
 brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]

RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=9403216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
 RT intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR PIR: G61033; G61033.
 DR InterPro: IPR002040; Tachy_Neurokinin.
 DR PROSITE: PS00267; TACHYKININ, 1.
 KM Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1086 MW; 3A3A407059D5BDC7 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HN 10
 DB 1 HN 2

Search completed: May 18, 2004, 10:02:34
 Job time : 6.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:55:20 ; Search time 30.25 Seconds
(without alignments)
125.164 Million cell updates/sec

Title: US-09-730-174a-5
Perfect score: 59
Sequence: 1 ANSEIQMLNNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 27 | 45.8 | 11 | 13 | Q9PS71 agkistron |
| 2 | 23 | 39.0 | 12 | 13 | P82081 limodynast |
| 3 | 20 | 33.9 | 8 | 13 | P82082 limodynast |
| 4 | 20 | 33.9 | 8 | 13 | P82083 limodynast |
| 5 | 20 | 33.9 | 12 | 13 | P82085 limodynast |
| 6 | 19 | 32.2 | 8 | 8 | Q34909 locusta mg |
| 7 | 19 | 32.2 | 9 | 12 | Q92766 canine dist |
| 8 | 19 | 32.2 | 9 | 12 | Q71066 canine dist |
| 9 | 18 | 30.5 | 8 | 10 | Q40659 cryza sativ |
| 10 | 18 | 30.5 | 10 | 12 | Q9PXC3 hepatic b |
| 11 | 18 | 30.5 | 11 | 5 | Q23876 dictyosteli |
| 12 | 18 | 30.5 | 12 | 15 | Q85631 avian carc |
| 13 | 17 | 28.8 | 7 | 6 | Q28742 erythrocyt |
| 14 | 17 | 28.8 | 9 | 4 | Q15891 homo sapien |
| 15 | 17 | 28.8 | 9 | 8 | Q9GD12 limospadix |
| 16 | 17 | 28.8 | 9 | 8 | Q9GCV6 sclerosperm |

| | | | | | | |
|----|----|------|----|----|--------|---------------------|
| 17 | 17 | 28.8 | 11 | 10 | P82336 | P82336 pistum sativ |
| 18 | 17 | 28.8 | 11 | 13 | Q9PS71 | Q9PS71 fugu rubrip |
| 19 | 16 | 27.1 | 8 | 3 | Q05403 | Q05403 saccharomyc |
| 20 | 16 | 27.1 | 8 | 4 | Q15894 | Q15894 homo sapien |
| 21 | 16 | 27.1 | 9 | 2 | Q44377 | Q44377 aeromonas t |
| 22 | 16 | 27.1 | 9 | 2 | Q44468 | Q44468 aeromonas v |
| 23 | 16 | 27.1 | 9 | 2 | Q8RKU3 | Q8RKU3 borrelia bu |
| 24 | 16 | 27.1 | 9 | 2 | Q43928 | Q43928 aeromonas p |
| 25 | 16 | 27.1 | 9 | 2 | Q44001 | Q44001 aeromonas e |
| 26 | 16 | 27.1 | 9 | 2 | Q9K4M6 | Q9K4M6 staphylococ |
| 27 | 16 | 27.1 | 9 | 10 | Q9FXL0 | Q9FXL0 lithium long |
| 28 | 16 | 27.1 | 10 | 2 | Q7WUG1 | Q7WUG1 pseudomonas |
| 29 | 16 | 27.1 | 10 | 10 | P82132 | P82132 spinacia ol |
| 30 | 16 | 27.1 | 10 | 10 | P82133 | P82133 spinacia ol |
| 31 | 16 | 27.1 | 10 | 13 | P82080 | P82080 limodynast |
| 32 | 16 | 27.1 | 12 | 2 | Q9X6Y0 | Q9X6Y0 aquifex pyr |
| 33 | 15 | 25.4 | 7 | 12 | Q66205 | Q66205 transistib |
| 34 | 15 | 25.4 | 8 | 13 | P82079 | P82079 limodynast |
| 35 | 15 | 25.4 | 9 | 2 | Q43960 | Q43960 azotobacter |
| 36 | 15 | 25.4 | 9 | 5 | Q8WRI9 | Q8WRI9 diosiphila |
| 37 | 15 | 25.4 | 10 | 6 | Q9TS43 | Q9TS43 sus scrofa |
| 38 | 15 | 25.4 | 10 | 8 | Q8WR7 | Q8WR7 chaitophoru |
| 39 | 15 | 25.4 | 11 | 6 | Q9BDC8 | Q9BDC8 pongo pygma |
| 40 | 15 | 25.4 | 11 | 6 | Q9BDQ9 | Q9BDQ9 gorilla gor |
| 41 | 15 | 25.4 | 11 | 6 | Q9BD00 | Q9BD00 pan troglod |
| 42 | 15 | 25.4 | 11 | 6 | Q9BDC9 | Q9BDC9 pan paniscu |
| 43 | 15 | 25.4 | 12 | 6 | Q9TQY5 | Q9TQY5 bos taurus |
| 44 | 15 | 25.4 | 12 | 11 | Q9ROV3 | Q9ROV3 mus musculu |
| 45 | 14 | 23.7 | 8 | 2 | Q49534 | Q49534 mycoplasma |

ALIGNMENTS

| | | | | |
|-----------------------|--|--------------|--------------------|-------------------------|
| RESULT 1 | Q9PS71 | PRELIMINARY; | PRT; | 11 AA. |
| AC | Q9PS71; | | | |
| DT | 01-MAY-2000 (TREMBlrel. 13, Created) | | | |
| DT | 01-MAY-2000 (TREMBlrel. 13, Last sequence update) | | | |
| DT | 01-JUN-2000 (TREMBlrel. 21, Last annotation update) | | | |
| DE | Fibrinolytic metalloproteinase (Fragment). | | | |
| OS | Agkistrodon contortrix. | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubridae; | | | |
| OC | Viperidae; Crotalinae; Agkistrodon. | | | |
| OX | NCBI_TaxID=8720; | | | |
| RN | [1] | | | |
| RP | SEQUENCE | | | |
| RK | MEDLINE=91378546; PubMed=1898066; | | | |
| RA | Guan A.L., Ketzius A.D., Henderson G.N., Markland F.S.Jr.; | | | |
| RT | "Purification and characterization of a fibrinolytic enzyme from venom | | | |
| RT | of the southern copperhead snake (Agkistrodon contortrix | | | |
| RT | contortrix)."; | | | |
| RL | Arch. Biochem. Biophys. 289:197-207 (1991). | | | |
| FT | NON_TER | | | |
| SO | SEQUENCE | 11 AA; | 1209 MW; | 7CA02D1D41B8772B CRC64; |
| Query Match | | 45.8%; | Score 27; | DB 13; |
| Best Local Similarity | | 71.4%; | Pred. No. 1.4e+02; | Length 11; |
| Matches | 5; | Conservative | 1; | Mismatches 1; |
| | | | | Indels 0; |
| | | | | Gaps 0; |
| QY | 6 QLMNNLG 12 | | | |
| DB | 4 ELGNLIG 10 | | | |
| RESULT 2 | P82081 | PRELIMINARY; | PRT; | 12 AA. |
| ID | P82081; | | | |
| AC | P82081; | | | |
| DT | 01-MAY-2000 (TREMBlrel. 13, Created) | | | |
| DT | 01-MAY-2000 (TREMBlrel. 13, Last sequence update) | | | |

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DYNASTIN 3.
OS Limnodynastes terraereginae (Northern banjo frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
NCBI_TaxID=104894;
RN
RN
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=TIBIAL GLAND;
RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT the banjo frogs Limnodynastes interioris, Limnodynastes dumerilii and
RT Limnodynastes terraereginae".
RL Aust. J. Chem. 46:833-842(1993).
CC -1- MASS SPECTROMETRY: MW=1236; METHOD=FAB.
SQ SEQUENCE 12 AA; 1236 MW; 147AA70FDF472724 CRC64;

Query Match 39.0%; Score 23; DB 13; Length 12;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 LHMNLG 12
|:|
|:|
|:|
Db 6 LHMNLG 11

RESULT 3
P82082 PRELIMINARY; PRT; 8 AA.
AC P82082;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DYNASTIN 4.
OS Limnodynastes salmini (Salmin's-striped frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
NCBI_TaxID=39404;
RN
RN
RN
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri".
RL Aust. J. Chem. 46:1235-1244(1993).
CC -1- MASS SPECTROMETRY: MW=772; METHOD=FAB.
SQ SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;

Query Match 33.9%; Score 20; DB 13; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LHMNLG 12
|:|
|:|
|:|
Db 2 LHMNLG 7

RESULT 4
P82083 PRELIMINARY; PRT; 8 AA.
AC P82083;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DYNASTIN 5.
OS Limnodynastes salmini (Salmin's-striped frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
NCBI_TaxID=39404;
RN
RN
RN

RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri".
RL Aust. J. Chem. 46:1235-1244(1993).
CC -1- MASS SPECTROMETRY: MW=786; METHOD=FAB.
SQ SEQUENCE 8 AA; 786 MW; 7B58772455B05728 CRC64;

QY 7 LHMNLG 12
|:|
|:|
|:|
Db 2 LHMNLG 7

RESULT 5
P82085 PRELIMINARY; PRT; 12 AA.
AC P82085;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DYNASTIN 7.
OS Limnodynastes salmini (Salmin's-striped frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
NCBI_TaxID=39404;
RN
RN
RN
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri".
RL Aust. J. Chem. 46:1235-1244(1993).
CC -1- MASS SPECTROMETRY: MW=1114; METHOD=FAB.
SQ SEQUENCE 12 AA; 1114 MW; 3AB5A976CAA72728 CRC64;

Query Match 33.9%; Score 20; DB 13; Length 12;
Best Local Similarity 66.7%; Pred. No. 4.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LHMNLG 12
|:|
|:|
|:|
Db 6 LHMNLG 11

RESULT 6
Q34909 PRELIMINARY; PRT; 8 AA.
AC Q34909;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
OS Locusta migratoria (Migratory locust).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
NCBI_TaxID=7004;
RN
RN
RN
RP SEQUENCE FROM N. A.
RX MEDLINE=88223478; PubMed=2836084;
RA McCracken A., Unruhusch I., Gellissen G.;
RT "Structure of the cloned Locusta migratoria mitochondrial genome:
RT restriction mapping and sequence of its ND-1 (URF-1) gene".
RL Curr. Genet. 11:625-630(1987).
DR EMBL; X05286; CAA28905.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.

```

KW Mitochondrion.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1019 MW; F8E3723304B45B6 CRC64;

Query Match
Best Local Similarity 32.2%; Score 19; DB 8; Length 8;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSBIOLMH 9
DB 1 MSYIKLKH 8

RESULT 7
ID 092766 PRELIMINARY; PRT; 9 AA.
AC 092766;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Dog #5526/89;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026237; AAC09167.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;

Query Match
Best Local Similarity 32.2%; Score 19; DB 12; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MEN 10
DB 1 MEN 3

RESULT 8
ID 071066 PRELIMINARY; PRT; 9 AA.
AC 071066;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Dog #10757/96;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026234; AAC09164.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;

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Query Match
Best Local Similarity 32.2%; Score 19; DB 12; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MEN 10
DB 1 MEN 3

RESULT 9
ID 040659 PRELIMINARY; PRT; 8 AA.
AC 040659;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Alpha-amylase (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91078641; PubMed=2258052;
RA Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA Rodriguez R.L.;
RT "Expression and secretion of rice alpha-amylase by saccharomyces
RT cerevisiae.";
RL Gene 94:209-216(1990).
DR EMBL; M62916; AAA33892.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;

Query Match
Best Local Similarity 30.5%; Score 18; DB 10; Length 8;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 5 IOLMNM 11
DB 1 IOLMNM 7

RESULT 10
ID 09PXC3 PRELIMINARY; PRT; 10 AA.
AC 09PXC3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE E antigen P208 (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE.
RX MEDLINE=92013147; PubMed=1717588;
RA Takasaki K., Kishimoto S., Ohori K., Yoshizawa H., Machida A.,
RA Ohnuma H., Tsuda F., Muneoka E., Miyakawa Y., Mayumi M.;
RT "Molecular heterogeneity of e antigen polypeptides in sera from
RT carriers of hepatitis B virus.";
RL J. Immunol. 147:3156-3160(1991).
DR PIR; B46453; B46453.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1238 MW; 485A6E3AE721B9C7 CRC64;

Query Match
Best Local Similarity 30.5%; Score 18; DB 12; Length 10;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 IOLMNM 9
DB 1 IOLMNM 9

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Db          1 MOLF 5

RESULT 11
Q23876      PRELIMINARY;      PRT;      11 AA.
AC Q23876;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
DE Actin 4.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
CX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82260445; PubMed=6286214;
RA McKewen M., Firtel R.A.;
RT "Actin multigene family of Dictyostelium.";
RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
DR EMBL; K02957; AAA33150.1; JOINED.
DR EMBL; K02956; AAA33150.1; JOINED.
SQ SEQUENCE 11 AA; 1205 MW; 728B4C14C6C2CAAB CRC64;

Query Match          30.5%; Score 18; DB 5; Length 11;
Best Local Similarity 28.6%; Pred. No. 9.9e+03;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY          4 EIOGMN 10
Db          5 DVQALNN 11

RESULT 12
Q85631      PRELIMINARY;      PRT;      12 AA.
AC Q85631;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE MH2, proviral DNA, myc to 3' LTR (Fragment).
OS Avian carcinoma virus.
OS Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
CX NCBI_TaxID=11958;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85033920; PubMed=6092695;
RA Surrave P., Jansen H.W., Bister K., Rapp U.R.;
RT "3'-terminal region of avian carcinoma virus MH2 shares sequence
  elements with avian sarcoma viruses Y73 and SR-A.";
RL J. Virol. 52:703-705(1984).
DR EMBL; K03100; AAA42388.1; -.
FT NON TER
SQ SEQUENCE 12 AA; 1466 MW; 72E4B884F30736DB CRC64;

Query Match          30.5%; Score 18; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 HNL 11
Db          2 HNL 4

RESULT 13
Q28742      PRELIMINARY;      PRT;      7 AA.
AC Q28742;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
  Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
  ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -.
DR PIR; I46868; I46868.
FT NON TER
SQ SEQUENCE 7 AA; 916 MW; 6B1B1A1E69326B0 CRC64;

Query Match          28.8%; Score 17; DB 6; Length 7;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          6 QLMN 10
Db          1 QKMD 5

RESULT 14
Q15891      PRELIMINARY;      PRT;      9 AA.
AC Q15891;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE (Clone XP2E8B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA Lee C.-C., Yarzani A., Wemert M., Bailey J., Couch L., Xiong M.,
  RA Coolbaugh M.I., Chnault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
  RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
  arrays cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32131; AAA73881.1; -.
FT NON TER
SQ SEQUENCE 9 AA; 1030 MW; B56635A1A33686D1 CRC64;

Query Match          28.8%; Score 17; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY          4 EIOGMN 12
Db          1 EHOAKTSLG 9

RESULT 15
Q9GD12      PRELIMINARY;      PRT;      9 AA.
AC Q9GD12;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Ribosomal protein S16 (Fragment).
RN RPS16.
OS Linospadix monostachya.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecoidae.

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OC Areceae; Liospadicinae; Liospadix.
OX NCBI_taxid=131282;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Amussen C.B.; Chase M.W.;
RT "Coding and noncoding plastid DNA in palm systematics."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: A0404941; CAC17917.1; -;
DR GO: GO:000507; Chloroplast; IEA.
KW Chloroplast.
FT NON TER 1 1
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1106 MW; 1B9236C2C041B50 CRC64;

Query Match 28.8%; Score 17; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e-06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IOLM 8
Db 6 VOLM 9

Search completed: May 18, 2004, 10:04:48
Job time : 31.25 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:42:39 ; Search time 45.75 Seconds
(without alignments)
74.111 Million cell updates/sec

Title: US-09-730-174A-5
Perfect score: 59
Sequence: 1 ANSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : A_Geneseq_29Jan04:*
Listing first 45 summaries

1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 53 | 89.8 | 11 | 3 | AAY96968 Parathyro |
| 2 | 50 | 84.7 | 11 | 6 | ABG72607 Parathyro |
| 3 | 50 | 84.7 | 12 | 6 | ABG72608 Parathyro |
| 4 | 46 | 78.0 | 10 | 2 | AAB91644 |
| 5 | 46 | 78.0 | 10 | 3 | AAY68767 Amino aci |
| 6 | 46 | 78.0 | 10 | 4 | AAB86219 Human par |
| 7 | 46 | 78.0 | 10 | 6 | ABR44166 Human par |
| 8 | 45 | 76.3 | 9 | 4 | AAB86225 Human par |
| 9 | 43.5 | 73.7 | 11 | 2 | AAY50600 Resin bou |
| 10 | 43 | 72.9 | 9 | 3 | AAB01862 PTH(1-14) |
| 11 | 43 | 72.9 | 9 | 3 | AAY96966 Parathyro |
| 12 | 40 | 67.8 | 9 | 2 | AAB91645 Human par |
| 13 | 40 | 67.8 | 9 | 3 | AAB01863 PTH(1-14) |
| 14 | 40 | 67.8 | 9 | 3 | AAY96961 Parathyro |
| 15 | 40 | 67.8 | 9 | 4 | AAB86220 Human par |
| 16 | 40 | 67.8 | 10 | 4 | AAB86932 Rat parat |
| 17 | 40 | 67.8 | 11 | 4 | AAB86931 Rat parat |
| 18 | 40 | 67.8 | 11 | 4 | AAB86935 Parathyro |
| 19 | 40 | 67.8 | 11 | 4 | AAB86931 Parathyro |
| 20 | 40 | 67.8 | 12 | 4 | AAB86914 Parathyro |
| 21 | 40 | 67.8 | 12 | 4 | AAB84769 Parathyro |
| 22 | 38 | 64.4 | 12 | 2 | AAB84765 Parathyro |
| 23 | 35 | 59.3 | 10 | 6 | ABP71484 Parathyro |
| 24 | 35 | 59.3 | 11 | 1 | AAB82547 (Asn10, T |
| 25 | 35 | 59.3 | 11 | 4 | AAB96892 Rat parat |

| | | | | | |
|----|----|------|----|---|--------------------|
| 26 | 35 | 59.3 | 11 | 6 | ABP71485 Parathyro |
| 27 | 35 | 59.3 | 11 | 6 | ABP71483 Parathyro |
| 28 | 35 | 59.3 | 12 | 4 | AAB96891 Rat parat |
| 29 | 35 | 59.3 | 12 | 6 | ABP71482 Parathyro |
| 30 | 33 | 55.9 | 9 | 3 | AAB01864 PTH(1-14) |
| 31 | 33 | 55.9 | 9 | 3 | AAY78849 Parathyro |
| 32 | 33 | 55.9 | 9 | 3 | AAY97062 PTH-rp N- |
| 33 | 32 | 54.2 | 8 | 2 | AAR91646 Human par |
| 34 | 32 | 54.2 | 8 | 3 | AAB07467 Antigenic |
| 35 | 32 | 54.2 | 9 | 4 | AAB86221 Human par |
| 36 | 30 | 50.8 | 9 | 3 | AAB01866 PTH(1-14) |
| 37 | 27 | 45.8 | 7 | 2 | AAR91647 Human par |
| 38 | 27 | 45.8 | 7 | 4 | AAB86222 Human par |
| 39 | 27 | 45.8 | 10 | 5 | ABG98580 F protein |
| 40 | 27 | 45.8 | 10 | 5 | ABG98582 F protein |
| 41 | 27 | 45.8 | 10 | 5 | ABG98581 F protein |
| 42 | 27 | 45.8 | 11 | 4 | ABU54029 Human DNA |
| 43 | 27 | 45.8 | 12 | 2 | AAR89301 Japanese |
| 44 | 27 | 45.8 | 12 | 2 | AAR64520 RP-2 pep |
| 45 | 27 | 45.8 | 12 | 3 | AAB21270 Fertilin |

ALIGNMENTS

RESULT 1
AAY96968
ID AAY96968 standard; peptide; 11 AA.
XX
AC AAY96968;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain (residues 1-11).
XX
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
XX bone reformation; resorption; remodeling; tether; osteoporosis.
XX
OS Homo sapiens.
XX
XX WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX
PS Claim 4; Page 92; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)-n-B, R1-S-(L)-n-R or S-(L)-n
-R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased theral activity, increasing CAMP

CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 11 AA;
Query Match 89.8%; Score 53; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AVSEIQMLMNL 11
1 AVSEIQMLMNL 11
DB 1 AVSEIQMLMNL 11
RESULT 2
ABG72607
ID ABG72607 standard; peptide; 11 AA.
XX
AC ABG72607;
XX
DT 11-FEB-2003 (first entry)
XX
DE Parathyroid hormone antigenic peptide 2-12.
XX
KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
XX
OS Homo sapiens.
OS Mus sp.
OS Rattus sp.
OS Bos taurus.
OS Sus scrofa.
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT Misc-difference 6 /label= Leu, Phe
FT
XX
PN US2002110871-A1.
XX
PD 15-AUG-2002.
XX
PF 05-DEC-2000; 2000US-00730174.
XX
PR 05-DEC-2000; 2000US-00730174.
XX
XX
PA (ZAHN/) ZAHRADNIK R J.
PA (LAVI/) LAVIGNE J R.
XX
PI Zahradnik RJ, Lavigne JR;
XX
DR WPI; 2003-066685/06.
XX
PT New parathyroid hormone (PTH) antigenic peptide inducing the formation
PT and isolation of antibodies having an affinity to it; useful for
PT determining bioactive PTH levels in serum, plasma and/or cell culture
PT media.
XX
XX
PS Claim 1; Page 5; 11pp; English.
XX
CC The invention relates to a new antigenic peptide for inducing the
CC formation and isolation of antibodies having an affinity to it, being
CC formed from the N-terminus of parathyroid hormone (PTH). Also included
CC are: (1) a method for producing antibodies useful in the determination of
CC PTH levels in a biological sample comprising: (a) providing at least one
CC first peptide antigen comprising a peptide fragment of PTH; (b)
CC administering the first peptide antigen to a host animal to induce
CC antibody production; (c) monitoring the antibody titre produced; (d)
CC isolating antisera produced in the host animal; and (e) selecting
CC antisera from the isolated antisera produced in the host that is capable
CC of binding to a second peptide antigen; (2) an antibody (ab) produced by

CC the method; and (3) test kits and analytical procedures used for the
CC determination of bioactive intact PTH utilizing (ab). The methods and
CC compositions of the present invention are useful for determining
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
CC
CC The antigens, antibodies and methods of the present invention, as
CC compared to prior art, have the particular advantages of possessing
CC greater affinity for PTH, and in particular, are designed to have a novel
CC recognition for amino acid residues extending beyond the first N-terminal
CC PTH residue, and further have negligible cross-reactivity with the large
CC non-molecular forms of PTH. PTH levels are an important parameter in
CC patients suffering from hypercalcaemia, osteoporosis and primary
CC hyperparathyroidism. The present sequence represents a PTH antigenic
CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,
CC canine and bovine PTH
XX
SQ Sequence 11 AA;
Query Match 84.7%; Score 50; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.012; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;
OY 2 VSEIQMLMNLG 12
1 VSEIQMLMNLG 11
DB 1 VSEIQMLMNLG 11
RESULT 3
ABG72608
ID ABG72608 standard; peptide; 12 AA.
XX
AC ABG72608;
XX
DT 11-FEB-2003 (first entry)
XX
DE Parathyroid hormone antigenic peptide 1-12.
XX
KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
XX
OS Homo sapiens.
OS Mus sp.
OS Rattus sp.
OS Bos taurus.
OS Sus scrofa.
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /label= Ser, Ala
FT Misc-difference 7 /label= Leu, Phe
FT
XX
PN US2002110871-A1.
XX
PD 15-AUG-2002.
XX
PF 05-DEC-2000; 2000US-00730174.
XX
PR 05-DEC-2000; 2000US-00730174.
XX
XX
PA (ZAHN/) ZAHRADNIK R J.
PA (LAVI/) LAVIGNE J R.
XX
PI Zahradnik RJ, Lavigne JR;
XX
DR WPI; 2003-066685/06.
XX
PT New parathyroid hormone (PTH) antigenic peptide inducing the formation
PT and isolation of antibodies having an affinity to it; useful for
PT determining bioactive PTH levels in serum, plasma and/or cell culture
PT media.
XX
XX
PS Claim 2; Page 5; 11pp; English.

XX The invention relates to a new antigenic peptide for inducing the
 CC formation and isolation of antibodies having an affinity to it, being
 CC formed from the N-terminus of parathyroid hormone (PTH). Also included
 CC are, (1) a method for producing antibodies useful in the determination of
 CC PTH levels in a biological sample comprising: (a) providing at least one
 CC first peptide antigen comprising a peptide fragment of PTH; (b)
 CC administering the first peptide antigen to a host animal to induce
 CC antibody production; (c) monitoring the antibody titre produced; (d)
 CC isolating antisera produced in the host animal, and (e) selecting
 CC antisera from the isolated antisera produced in the host that is capable
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by
 CC the method; and (3) test kits and analytical procedures used for the
 CC determination of bioactive intact PTH utilising (ab). The methods and
 CC compositions of the present invention are useful for determining
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
 CC The antigens, antibodies and methods of the present invention, as
 CC compared to prior art, have the particular advantages of possessing
 CC greater affinity for PTH, and in particular, are designed to have a novel
 CC recognition for amino acid residues extending beyond the first N-terminal
 CC PTH residue, and further have negligible cross-reactivity with the large
 CC non-molecular forms of PTH. PTH levels are an important parameter in
 CC patients suffering from hypercalcaemia, osteoporosis and primary
 CC hyperparathyroidism. The present sequence represents a PTH antigenic
 CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,
 CC canine and bovine PTH

XX Sequence 12 AA;
 SQ

Query Match 84.7%; Score 50; DB 6; Length 12;
 Best Local Similarity 90.9%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSEIQMLNIG 12
 Db 2 VSSEIQMLNIG 12

RESULT 4
 AAR91644
 ID AAR91644 standard; peptide; 10 AA.
 AC AAR91644;
 XX 06-NOV-1996 (first entry)
 DT Human parathyroid hormone antigenic peptide hPTH 1-10.
 DE Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
 KM diagnosis; active hPTH 1-37.
 XX Synthetic.
 OS DE4434551-A1.
 PN 04-APR-1996.
 PD 28-SEP-1994; 94DE-04434551.
 PF 28-SEP-1994; 94DE-04434551.
 PR 28-SEP-1994; 94DE-04434551.
 PA (FORS/) FORSSMANN W.
 XX (FORS/) FORSSMANN W.
 PI Adermann K, Forsmann W, Hock D, Maegerlein M;
 XX WPI; 1996-180391/19.
 DR New antigenic peptide(s) from human parathyroid hormone - and antibodies
 PT generated using them, able to distinguish between active and inactive
 PT forms of the hormone.
 PS Claim 2; Page 4; 5pp; German.
 XX

CC The present sequence is a specific example of claimed immunogenic
 CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
 CC terminal alpha-helical region and/or the non-structured region of the
 CC hormone. Antibodies and their binding fragments generated by injecting an
 CC animal with the peptides are useful as diagnostic reagents for
 CC determination of biologically active hPTH(1-37)

XX Sequence 10 AA;
 SQ

Query Match 78.0%; Score 46; DB 2; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.061;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQMLNHN 10
 Db 1 AVSEIQMLNHN 10

RESULT 5
 AAY68767
 ID AAY68767 standard; peptide; 10 AA.
 AC AAY68767;
 XX 05-MAY-2000 (first entry)
 DT Amino acids 1-10 of a parathyroid hormone (PTH).
 DE Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;
 XX slimming treatment; cellulite; skin firming.
 KW Unidentified.
 OS WO200004047-A1.
 PN 27-JAN-2000.
 PD 07-JUL-1999; 99MO-FR001687.
 PE 17-JUL-1998; 98FR-00009193.
 PR (SEDE-) SEDERMA.
 PA Lintner K;
 XX WPI; 2000-171243/15.
 DR New parathyroid hormone fragment peptides, used as lipolysis stimulants
 PT in topically applied cosmetic compositions for slimming treatment of
 PT excessive weight in hips and thighs.
 XX Claim 1; Page 8; 18pp; French.
 PS The present sequence represents a parathyroid hormone (PTH) fragment,
 CC comprising amino acids 1-10. Parathyroid hormone fragments of the
 CC invention have lipolytic stimulating activity (especially when topically
 CC administered). The lipolytic activity of the peptides is enhanced when
 CC they are chemically modified to increase their lipophilicity. The
 CC peptides are used in cosmetic or dermatological compositions for skin
 CC care. They are especially used for slimming treatment of excessive weight
 CC in the thighs and hips, in the treatment of cellulite and for skin
 CC firming

XX Sequence 10 AA;
 SQ

Query Match 78.0%; Score 46; DB 3; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.061;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQMLNHN 10
 Db 1 AVSEIQMLNHN 10

RESULT 6
 AAB86219 standard; peptide; 10 AA.
 AAB86219;
 03-SEP-2001 (first entry)
 Human parathyroid hormone immunogenic peptide SEQ ID 1.
 Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
 diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
 hypo-parathyroidism; hyper-parathyroidism.
 Homo sapiens.
 DE19961350-A1.
 21-JUN-2001.
 17-DEC-1999; 99DE-01061350.
 17-DEC-1999; 99DE-01061350.
 17-DEC-1999; 99DE-01061350.
 (IMMU-) IMMUNDIAGNOSTIK AG.
 Armbruster FP;
 WPI: 2001-376318/40.
 Determining the content of physiologically active parathyroid hormone,
 useful in diagnosis of calcium-metabolism disorders, using two antibodies
 reactive with different epitopes.
 Disclosure; Page 3; 10pp; German.
 This invention describes a novel method for determining (M1) the content
 of active parathyroid hormone (A) by treating a sample with (i) antibody
 (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
 and including the N-terminal residue and (ii) antibody (Ab2) that
 recognizes an epitope within the receptor-binding site of (A). The number
 of molecules that react with both antibodies is determined and used to
 calculate the content of physiologically active (A). The method is used
 for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
 hyper-parathyroidism. The method (unlike known assays) recognizes that
 (i) some fragments of (A) shorter than the complete (84 aa) peptide are
 active and (ii) that apparently intact peptide may be biologically
 inactive, and also takes into account the fact that some fragments of (A)
 are antagonistic (these have the receptor-binding site but lack the N-
 terminus). It thus provides a true measure of the content of
 physiologically active (A); contrast methods that measure intact peptide
 and its 1-37 fragment which may produce falsely high values. This
 sequence represents a peptide fragment used to illustrate the method of
 the invention
 Sequence 10 AA:
 Query Match 78.0%; Score 46; DB 4; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.061; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0;
 1 AVSEIQLMHN 10
 1 SVSEIQLMHN 10
 DB 1 SVSEIQLMHN 10
 RESULT 7
 ABR44166 standard; peptide; 10 AA.
 ABR44166;
 ABR44166;

DT 04-AUG-2003 (first entry)
 DE Human parathyroid hormone (hPTH) fragment (residues 1-10).
 XX Fusion peptide; cat: hPTHDP; parathyroid hormone; skin; cosmetic;
 XX lipolysis; human; hPTH.
 XX Homo sapiens.
 OS WO2003035697-A1.
 XX 01-MAY-2003.
 XX 06-MAY-2002; 2002WO-KR000835.
 XX 27-SEP-2001; 2001KR-00060245.
 XX 15-MAR-2002; 2002KR-00014062.
 XX (GLDS) LG HOUSEHOLD & HEALTH CARE LTD.
 PA Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H;
 PI Chang M;
 PI WPI: 2003-468288/44.
 DR Novel fusion peptide comprising self cell-penetrating Tat peptide bound
 PT to human parathyroid hormone-derived peptide, useful as component of skin
 PT slimming cosmetic composition.
 XX Claim 5; Page 6; 32pp; English.
 The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-
 CC penetrating Tat peptide is bound to human parathyroid hormone-derived
 CC peptide (hPTHDP). The fusion peptide is useful as a component of skin
 CC slimming cosmetic composition. The fusion peptide does not cause
 CC irritation, easily and safely penetrates into integument and endothelium,
 CC does not cause skin disease and has superior lipolysis effects, and is
 CC durable. The present sequence represents a human parathyroid hormone
 CC (hPTH) fragment that can be used to construct the fusion peptide
 XX
 SQ Sequence 10 AA:
 Query Match 78.0%; Score 46; DB 6; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.061; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0;
 1 AVSEIQLMHN 10
 1 SVSEIQLMHN 10
 DB 1 SVSEIQLMHN 10
 RESULT 8
 AAB86225 standard; peptide; 9 AA.
 AAB86225;
 03-SEP-2001 (first entry)
 Human parathyroid hormone immunogenic peptide SEQ ID 7.
 Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
 diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
 hypo-parathyroidism; hyper-parathyroidism.
 Homo sapiens.
 DE19961350-A1.
 21-JUN-2001.
 17-DEC-1999; 99DE-01061350.

PR 17-DEC-1999; 99DE-01061350.
 XX (IMMU-) IMMUNODIAGNOSTIK AG.
 XX Armbruster FP;
 PI WPI; 2001-376318/40.
 DR
 XX
 PT Determining the content of physiologically active parathyroid hormone,
 PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
 PT reactive with different epitopes.
 XX
 XX Disclosure; Page 3; 10pp; German.
 CC This invention describes a novel method for determining (M1) the content
 CC of active parathyroid hormone (A) by treating a sample with (i) antibody
 CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
 CC and including the N-terminal residue and (ii) antibody (Ab2) that
 CC recognizes an epitope within the receptor-binding site of (A). The number
 CC of molecules that react with both antibodies is determined and used to
 CC calculate the content of physiologically active (A). The method is used
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that
 CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
 CC active and (ii) that apparently intact peptide may be biologically
 CC inactive, and also takes into account the fact that some fragments of (A)
 CC are antagonistic (these have the receptor-binding site but lack the N-
 CC terminus). It thus provides a true measure of the content of
 CC physiologically active (A); contrast methods that measure intact peptide
 CC and its 1-37 fragment which may produce falsely high values. This
 CC sequence represents a peptide fragment used to illustrate the method of
 CC the invention
 CC
 XX Sequence 9 AA;
 SQ
 Query Match 76.3%; Score 45; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VSEIQIMEN 10
 DB 1 VSEIQIMEN 9
 RESULT 9
 AAY50600
 ID AAY50600 standard; peptide; 11 AA.
 XX
 AC AAY50600;
 XX
 XX 09-FEB-2000 (first entry)
 DT
 XX
 XX Resin bound cyclic peptide 33.
 DE
 XX
 XX Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;
 KW hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;
 KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;
 KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 1
 FT /note= "FMOC-Ala"
 FT
 FT Misc-difference 3
 FT /note= "Ser(OtBu)"
 FT
 FT Misc-difference 4
 FT /note= "Glu(OtBu)"
 FT
 FT Misc-difference 6
 FT /note= "Gln(Trt)"
 FT
 FT Misc-difference 9
 FT /note= "His(Trt)"
 FT
 FT Misc-difference 10

FT /note= "Asn(Trt)"
 XX
 XX WO9952933-A1.
 PN
 XX 21-OCT-1999.
 PD
 XX
 XX 15-APR-1999; 99WO-US008435.
 PF
 XX
 XX 15-APR-1998; 98US-0081997P.
 PR
 XX (RHON) RHONE-POULENC ROGER PHARM INC.
 PA
 XX
 PI Sledeski AM, Mancel JJ;
 PS WPI; 1999-633822/54.
 DR
 XX
 XX Convergent synthesis of peptides for treating e.g. bone disorders.
 PT
 PT Disclosure; Page 75; 85pp; English.
 PS
 XX This invention describes a novel method for the preparation of peptides
 CC (ii) that contain both cyclic and linear peptide fragments comprises
 CC sequential reaction of a resin-bound linear fragment with the cyclic
 CC fragment in N-protected form and optionally other linear fragments. The
 CC products of the invention have osteopathic and hypotensive activity. (ii)
 CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The
 CC method is particularly used to prepare cyclic peptide analogs of
 CC parathyroid hormone (PTH) or PTH-related peptides which are useful for
 CC treating diseases that respond to treatment with agents that bind to PTH
 CC receptors (with or without activation of adenyllyl cyclase activity), e.g.
 CC hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-
 CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also
 CC for promoting repair of bone fractures. Separate synthesis of the cyclic
 CC fragment allows convergent synthesis of resin-bound (ii), with better
 CC yields and higher throughput. The difficulties associated with
 CC preparation of the bridged fragment are confined to a small peptide which
 CC can be purified before reaction with the resin-bound component. AAY5060-
 CC Y50614 represent the peptide fragments described in the method of the
 CC invention
 CC
 XX Sequence 11 AA;
 SQ
 Query Match 73.7%; Score 43.5; DB 2; Length 11;
 Best Local Similarity 91.7%; Pred. No. 0.2;
 Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 AVSEIQIMHNG 12
 DB 1 AVSEIQIMHNG 11
 RESULT 10
 AAB01862
 ID AAB01862 standard; peptide; 9 AA.
 XX
 AC AAB01862;
 XX
 XX 11-SEP-2000 (first entry)
 DT
 XX
 XX PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.
 DE
 XX
 XX Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
 KW calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
 KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 PN WO200023594-A1.
 XX
 XX 27-APR-2000.
 PD
 XX
 XX 20-OCT-1999; 99WO-US024481.

| | | |
|----|--|-------------------------------------|
| XX | 22-OCT-1998; | 98US-0105530P. |
| XX | | |
| PR | (GARD/) | GARDELLA T J. |
| PA | (KRON/) | KRONENBERG H M. |
| PA | (POT/) | POTTS J T. |
| PA | (JUEP/) | JUEPNER H. |
| PI | Gardella TJ, | Kronenberg HM, Potts JT, Juepner H; |
| XX | WPI; 2000-339693/29. | |
| DR | | |
| XX | | |
| PT | Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic | |
| PT | acids that encode them, useful for treating osteoporosis. | |
| XX | | |
| PS | Disclosure; Page 26, 73pp; English. | |
| XX | | |
| CC | The invention relates to a novel parathyroid hormone (PTH) peptide | |
| CC | (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and | |
| CC | biologically active derivatives thereof (AAB01857-B01858, AAB01861- | |
| CC | B01863). The peptides of the invention are at least 85% identical to the | |
| CC | generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Ileu-X3-His-X4-X5- | |
| CC | Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is | |
| CC | Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser; | |
| CC | provided that the peptide is not PTHrP(1-14). The peptides of the | |
| CC | invention also encompass fragments of peptides of the invention | |
| CC | consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C- | |
| CC | terminal derivatives. PTH is a major regulator of calcium homeostasis, | |
| CC | and is necessary for the normal function of the gastrointestinal, | |
| CC | skeletal, neurological system, neuromuscular and cardiovascular systems. | |
| CC | It binds to both PTH-1 receptors on osteoblasts and renal tubular cells, | |
| CC | and to the recently identified PTH-2 receptor. PTH has a potent anabolic | |
| CC | effect on the skeleton, and mediates calcium reabsorption, enhances | |
| CC | phosphate clearance and vitamin D synthesis in the kidney. A homologous | |
| CC | calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of | |
| CC | the renal and skeletal actions of PTH, and also bind to the PTH-1 | |
| CC | receptor. They do not bind to the PTH-2 receptor. The peptides of the | |
| CC | invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858, | |
| CC | AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867- | |
| CC | B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of | |
| CC | osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for the treatment of | |
| CC | osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating | |
| CC | medical disorders that arise from excessive or altered action of the PTH- | |
| CC | 1/PTH-2 receptor. Detectably labeled peptides of the invention are also | |
| CC | useful in the determination of rates of bone formation, bone resorption | |
| CC | and/or bone remodelling in a patient. The peptides of the invention are | |
| CC | "humanised" versions of PTH or PTHrP which are inexpensive to prepare by | |
| CC | conventional synthetic chemistry, and can be delivered to a patient via | |
| CC | non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent | |
| CC | PTH-1/PTH-2 receptor agonists | |
| CC | | |
| XX | | |
| SQ | Sequence 9 AA: | |
| | Query Match 72.9%; Score 43; DB 3; Length 9; | |
| | Best Local Similarity 100.0%; Pred. No. 1.4e+06; | |
| | Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0. | |
| QY | 1 AVSEIQLMH 9 | |
| | | |
| | 1 AVSEIQLMH 9 | |
| DB | | |
| ID | AAV96966 standard; peptide; 9 AA. | |
| XX | AAV96966 | |
| XX | AAV96966; | |
| DT | 31-OCT-2000 (first entry) | |
| XX | | |
| DE | Parathyroid hormone N-terminal signaling domain (residues 1-9). | |
| XX | | |
| XX | PTH; parathyroid hormone; N-terminal; signaling domain; bone mass; | |

```

XX bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
XX Homo sapiens.
XX
XX WO200039278-A2.
XX
XX 06-Jul-2000.
XX
XX 30-DEC-1999; 59WC-US031108.
XX
XX 31-DEC-1998; 98US-0114577P.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI, 2000-452384/39.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass.
XX
XX Claim 4; Page 92; 119p; English.
XX
XX Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or S-(L) n
XX -R, are new. S is an amino terminal signaling functional domain of
XX parathyroid hormone (PTH); L is a linker molecule present n times, (where
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the
XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
XX sequence. The new compounds are used for treating mammalian conditions
XX characterized by decreases in bone mass, determining rates of bone
XX reformation, bone resorption and/or bone remodeling, treating diseases
XX and disorders associated with decreased tether1 activity, increasing cAMP
XX in a mammalian cell having PTH-1 receptors, or screening for a peptide or
XX non-peptide PTH (claimed). The new compound can be administered by
XX inhalation unlike the large native PTH or PTHrp which avoids the need for
XX regular injections to treat osteoporosis
XX
XX Sequence 9 AA.
XX
XX Query Match 72.9%; Score 43; DB 3; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1,4e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX 1 AVSEIQLMH 9
XX |||||
XX 1 AVSEIQLMH 9
XX
XX RESULT 12
XX AAR91645
XX AAR91645 standard; peptide; 9 AA.
XX
XX AAR91645;
XX
XX 06-NOV-1996 (first entry)
XX
XX Human parathyroid hormone antigenic peptide hPTH 1-9.
XX
XX Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
XX diagnosis; active hPTH 1-37.
XX
XX Synthetic.
XX
XX DE4434551-A1.
XX
XX 04-APR-1996.
XX
XX 28-SEP-1994; 94DE-04434551.

```

XX 28-SEP-1994; 94DE-04434551.
XX (FORS/) FORSSMANN W.
XX Adermann K, Forssmann W, Hock D, Maegerlein M;
XX WPI; 1996-180391/19.
XX
XX New antigenic peptide(s) from human parathyroid hormone - and antibodies
XX generated using them, able to distinguish between active and inactive
XX forms of the hormone.
XX
XX Claim 2; Page 4; 5pp; German.
XX
XX The present sequence is a specific example of claimed immunogenic
XX peptides having a sequence from hPTH(1-37) which includes the N- or C-
XX terminal alpha-helical region and/or the non-structured region of the
XX hormone. Antibodies and their binding fragments generated by injecting an
XX animal with the peptides are useful as diagnostic reagents for
XX determination of biologically active hPTH(1-37)
XX
XX Sequence 9 AA;
SO
Query Match 67.8%; Score 40; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AVSEIQLMH 9
Db 1 SVSEIQLMH 9
RESULT 13
AAB01863
ID AAB01863 standard; peptide; 9 AA.
XX
AC AAB01863;
XX
XX 11-SEP-2000 (first entry)
XX PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.
XX
XX Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
XX calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
XX bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS Homo sapiens.
XX Synthetic.
XX
XX WO200023594-A1.
XX
XX 27-APR-2000.
XX
XX 20-OCT-1999; 99WO-US024481.
XX
XX 22-OCT-1998; 98US-0105530P.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX Gardella T, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-339693/29.
XX
XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
XX acids that encode them, useful for treating osteoporosis.
XX
XX Disclosure; Page 26; 73pp; English.
XX
XX The invention relates to a novel parathyroid hormone (PTH) peptide

CC (AAB01859) and parathyroid hormone-related peptide (PTHrP, AAB01860), and
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC B01863). The peptides of the invention are at least 85% identical to the
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC provided that the peptide is not PTHrP(1-14). The peptides of the
CC invention also encompass fragments of peptides of the invention
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC and is necessary for the normal function of the gastrointestinal systems,
CC skeletal, neurological system, neuromuscular and cardiovascular systems.
CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC effect on the skeleton, and mediates calcium reabsorption, enhances
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous
CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC the renal and skeletal actions of PTH, and also bind to the PTH-1
CC receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC conditions characterised by a decrease in bone mass, such as
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC medical disorders that arise from excessive or altered action of the PTH-
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC useful in the determination of rates of bone formation, bone resorption
CC and/or bone remodelling in a patient. The peptides of the invention are
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC conventional synthetic chemistry, and can be delivered to a patient via
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC PTH-1/PTH-2 receptor agonists
XX
XX Sequence 9 AA;
SO
Query Match 67.8%; Score 40; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AVSEIQLMH 9
Db 1 AVSEIQLMH 9
RESULT 14
AAY96981
ID AAY96981 standard; peptide; 9 AA.
XX
AC AAY96981;
XX
XX 31-OCT-2000 (first entry)
XX
XX Parathyroid hormone N-terminal signalling domain.
XX
XX PTH; parathyroid hormone; N-terminal; signalling domain; bone mass;
XX bone reformation; resorption; remodeling; tether; osteoporosis.
XX
OS Homo sapiens.
XX
XX WO200039278-A2.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US031108.
XX
XX 31-DEC-1998; 98US-0114577P.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX Gardella T, Kronenberg HM, Potts JT, Jueppner H;

XX
DR MPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 11; Page 93; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)-n-B, R-1-S-(L)-n-R or S-(L)-n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R-1 is the
CC PTH-1 receptor signal sequence; and R is a portion of PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased reformation activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrp which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 9 AA;
XX
Query Match 67.8%; Score 40; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AVSEIQLMH 9
Db 1 SVSEIQLMH 9
XX
RESULT 15
AAB86220
ID AAB86220 standard; peptide; 9 AA.
XX
AC AAB86220;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human parathyroid hormone immunogenic peptide SEQ ID 2.
XX
KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW hypo-parathyroidism; hyper-parathyroidism.
XX
OS Homo sapiens.
XX
DEI961350-A1.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99DE-01061350.
XX
PR 17-DEC-1999; 99DE-01061350.
XX
PA (IMMU-) IMMUNODIAGNOSTIK AG.
XX
PI Ambruster FP;
XX
DR MPI; 2001-376318/40.
XX
PT Determining the content of physiologically active parathyroid hormone,
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT reactive with different epitopes.
XX
PS Disclosure; Page 3; 10pp; German.
XX
CC This invention describes a novel method for determining (M1) the content
CC of active parathyroid hormone (A) by treating a sample with (1) antibody

CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (11) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyper-parathyroidism. The method (unlike known assays) recognizes that
CC (1) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (11) that apparently intact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention
XX
SQ Sequence 9 AA;
XX
Query Match 67.8%; Score 40; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AVSEIQLMH 9
Db 1 SVSEIQLMH 9
XX
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Job time : 45.75 secs

Tue May 18 12:03:07 2004

us-09-730-174a-5.closed.rapb

Page 1

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OM protein - protein search, using sw model

Run on: May 18, 2004, 10:04:51 ; Search time 33.25 Seconds
(without alignments)

100.425 Million cell updates/sec

Title: US-09-730-174A-5

Perfect score: 59

Sequence: 1 AVSEIQMLHNLG 12

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Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 166097

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 59 | 100.0 | 12 | 9 | US-09-730-174A-5 | Sequence 5, Appli |
| 2 | 56 | 94.9 | 12 | 9 | US-09-730-174A-3 | Sequence 3, Appli |
| 3 | 55 | 93.2 | 11 | 9 | US-09-730-174A-1 | Sequence 1, Appli |
| 4 | 55 | 93.2 | 12 | 9 | US-09-730-174A-6 | Sequence 4, Appli |
| 5 | 52 | 88.1 | 12 | 9 | US-09-730-174A-2 | Sequence 2, Appli |
| 6 | 51 | 86.4 | 11 | 9 | US-09-730-174A-2 | Sequence 1, Appli |
| 7 | 46 | 78.0 | 10 | 14 | US-10-168-185-7 | Sequence 7, Appli |
| 8 | 45 | 76.3 | 9 | 14 | US-10-168-185-7 | Sequence 6, Appli |
| 9 | 43 | 72.3 | 8 | 14 | US-10-168-185-8 | Sequence 8, Appli |
| 10 | 41 | 69.5 | 8 | 14 | US-10-168-185-8 | Sequence 7, Appli |
| 11 | 40 | 67.8 | 9 | 14 | US-10-168-185-2 | Sequence 2, Appli |
| 12 | 40 | 67.8 | 9 | 14 | US-10-168-185-2 | Sequence 8, Appli |
| 13 | 33 | 55.9 | 8 | 14 | US-10-168-185-3 | Sequence 3, Appli |
| 14 | 32 | 54.2 | 8 | 14 | US-10-168-185-3 | Sequence 10, Appli |
| 15 | 30 | 50.8 | 9 | 14 | US-10-168-185-3 | Sequence 10, Appli |

| | | | | | | |
|----|----|------|----|----|-------------------|--------------------|
| 16 | 28 | 47.5 | 12 | 14 | US-10-319-130-16 | Sequence 16, Appli |
| 17 | 27 | 45.8 | 7 | 14 | US-10-168-185-4 | Sequence 4, Appli |
| 18 | 26 | 44.1 | 10 | 14 | US-10-033-741-61 | Sequence 61, Appli |
| 19 | 25 | 42.4 | 9 | 9 | US-09-746-945-6 | Sequence 6, Appli |
| 20 | 25 | 42.4 | 11 | 12 | US-09-747-287-185 | Sequence 185, App |
| 21 | 24 | 40.7 | 10 | 9 | US-09-826-290-27 | Sequence 27, Appli |
| 22 | 24 | 40.7 | 10 | 16 | US-10-264-309-369 | Sequence 369, App |
| 23 | 24 | 40.7 | 11 | 12 | US-10-609-217-41 | Sequence 41, Appli |
| 24 | 24 | 40.7 | 11 | 12 | US-10-632-388-41 | Sequence 41, Appli |
| 25 | 24 | 40.7 | 11 | 12 | US-10-651-723-41 | Sequence 41, Appli |
| 26 | 24 | 40.7 | 11 | 12 | US-10-645-751-41 | Sequence 41, Appli |
| 27 | 24 | 40.7 | 11 | 16 | US-10-666-686-41 | Sequence 41, Appli |
| 28 | 24 | 40.7 | 11 | 16 | US-10-653-048-41 | Sequence 41, Appli |
| 29 | 24 | 40.7 | 12 | 14 | US-10-286-457-294 | Sequence 294, App |
| 30 | 23 | 39.0 | 6 | 14 | US-10-168-185-5 | Sequence 5, Appli |
| 31 | 23 | 39.0 | 7 | 14 | US-10-286-457-469 | Sequence 469, App |
| 32 | 23 | 39.0 | 7 | 15 | US-10-368-280-12 | Sequence 12, Appli |
| 33 | 23 | 39.0 | 7 | 15 | US-10-374-038-12 | Sequence 12, Appli |
| 34 | 23 | 39.0 | 9 | 9 | US-09-894-018-332 | Sequence 332, App |
| 35 | 23 | 39.0 | 9 | 10 | US-09-821-734-4 | Sequence 4, Appli |
| 36 | 23 | 39.0 | 9 | 10 | US-09-854-248-11 | Sequence 11, Appli |
| 37 | 23 | 39.0 | 9 | 12 | US-10-253-286-288 | Sequence 288, App |
| 38 | 23 | 39.0 | 9 | 14 | US-10-094-699-50 | Sequence 50, Appli |
| 39 | 23 | 39.0 | 9 | 15 | US-10-117-937-249 | Sequence 249, App |
| 40 | 23 | 39.0 | 9 | 15 | US-10-117-937-249 | Sequence 288, App |
| 41 | 23 | 39.0 | 10 | 14 | US-10-094-699-49 | Sequence 49, Appli |
| 42 | 23 | 39.0 | 10 | 14 | US-10-232-187-8 | Sequence 8, Appli |
| 43 | 23 | 39.0 | 10 | 14 | US-10-168-185-11 | Sequence 11, Appli |
| 44 | 23 | 39.0 | 10 | 15 | US-10-026-066-31 | Sequence 31, Appli |
| 45 | 23 | 39.0 | 15 | 15 | US-10-026-066-83 | Sequence 83, Appli |

ALIGNMENTS

RESULT 1
US-09-730-174A-5
Sequence 5, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
APPLICANT: ZentradiK, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
FILE REFERENCE: IMUNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 5
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5

Query Match 100.0%; Score 59; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQMLHNLG 12
DB 1 AVSEIQMLHNLG 12

RESULT 2
US-09-730-174A-3
Sequence 3, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
APPLICANT: ZentradiK, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
FILE REFERENCE: IMUNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 5
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3

```

; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3
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```

Query Match          94.8%; Score 56; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0022;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```

QY      1 AVSEIQLMNHLG 12
       : ||||| |||||
Db      1 SVSEIQLMNHLG 12
```

```

RESULT 3
US-09-730-174A-1
; Sequence 1, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: INJUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1
```

```

Query Match          93.2%; Score 55; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY      2 VSEIQLMNHLG 12
       : ||||| |||||
Db      1 VSEIQLMNHLG 11
```

```

RESULT 4
US-09-730-174A-6
; Sequence 6, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: INJUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-6
```

```

Query Match          93.2%; Score 55; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

QY      1 AVSEIQLMNHLG 12
       : ||||| |||||
Db      1 AVSEIQLMNHLG 12
```

```

RESULT 5
US-09-730-174A-4
; Sequence 4, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: INJUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4
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```

Query Match          88.1%; Score 52; DB 9; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.011;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```

QY      1 AVSEIQLMNHLG 12
       : ||||| |||||
Db      1 SVSEIQLMNHLG 12
```

```

RESULT 6
US-09-730-174A-2
; Sequence 2, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: INJUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-2
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```

Query Match          86.4%; Score 51; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      2 VSEIQLMNHLG 12
       : ||||| |||||
Db      1 VSEIQFMNHLG 11
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```

RESULT 7
US-10-168-185-1
; Sequence 1, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Mischlicker, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
```

;; TITLE OF INVENTION: Activity in a Human Sample
;; FILE REFERENCE: HLZ-004US
;; CURRENT APPLICATION NUMBER: US/10/168,185
;; CURRENT FILING DATE: 2002-06-17
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911
;; PRIOR FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: DE 19961350
;; PRIOR FILING DATE: 1999-12-17
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-168-185-1

Query Match 78.0%; Score 46; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVESEIQLMHN 10
DB 1 SVSEIQLMHN 10

RESULT 8
US-10-168-185-7
;; Sequence 7, Application US/10/168185
;; Publication No. US20030175802A1
;; GENERAL INFORMATION:
;; APPLICANT: Armbruster, Franz Paul
;; APPLICANT: Mischichler, Albert
;; APPLICANT: Schmidt-Gayk, Heinrich
;; APPLICANT: Roth, Heinz-Jürgen
;; TITLE OF INVENTION: Method for Determining Parathormone
;; TITLE OF INVENTION: Activity in a Human Sample
;; FILE REFERENCE: HLZ-004US
;; CURRENT APPLICATION NUMBER: US/10/168,185
;; CURRENT FILING DATE: 2002-06-17
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911
;; PRIOR FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: DE 19961350
;; PRIOR FILING DATE: 1999-12-17
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 7
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-168-185-7

Query Match 76.3%; Score 45; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHN 10
DB 1 VSEIQLMHN 9

RESULT 9
US-10-192-673-6
;; Sequence 6, Application US/10/192673
;; Publication No. US20030166838A1
;; GENERAL INFORMATION:
;; APPLICANT: Gardella, Thomas J.
;; APPLICANT: Kronenberg, Henry
;; APPLICANT: Potts, John T.
;; APPLICANT: Juppner, Harald
;; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;; FILE REFERENCE: 0609.4570002

;; CURRENT APPLICATION NUMBER: US/10/192,673
;; CURRENT FILING DATE: 2002-07-11
;; PRIOR APPLICATION NUMBER: U.S. 09/421,379
;; PRIOR FILING DATE: 1999-10-20
;; PRIOR APPLICATION NUMBER: U.S. 60/105,530
;; PRIOR FILING DATE: 1998-10-22
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-192-673-6

Query Match 72.9%; Score 43; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVESEIQLMH 9
DB 1 AVESEIQLMH 9

RESULT 10
US-10-168-185-8
;; Sequence 8, Application US/10/168185
;; Publication No. US20030175802A1
;; GENERAL INFORMATION:
;; APPLICANT: Armbruster, Franz Paul
;; APPLICANT: Mischichler, Albert
;; APPLICANT: Schmidt-Gayk, Heinrich
;; APPLICANT: Roth, Heinz-Jürgen
;; TITLE OF INVENTION: Method for Determining Parathormone
;; TITLE OF INVENTION: Activity in a Human Sample
;; FILE REFERENCE: HLZ-004US
;; CURRENT APPLICATION NUMBER: US/10/168,185
;; CURRENT FILING DATE: 2002-06-17
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911
;; PRIOR FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: DE 19961350
;; PRIOR FILING DATE: 1999-12-17
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-168-185-8

Query Match 69.5%; Score 41; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQLMHN 10
DB 1 SEIQLMHN 8

RESULT 11
US-10-192-673-7
;; Sequence 7, Application US/10/192673
;; Publication No. US20030166838A1
;; GENERAL INFORMATION:
;; APPLICANT: Gardella, Thomas J.
;; APPLICANT: Kronenberg, Henry
;; APPLICANT: Potts, John T.
;; APPLICANT: Juppner, Harald
;; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)


```
FILE REFERENCE: 0609.4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-10-192-673-7
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```
Query Match      67.8%  Score 40; DB 14; Length 9;
Best Local Similarity 88.9%  Pred. No. 1e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AVSEIQLMH 9
      : |||||:|
Db      1 SVSEIQLMH 9
```

```
RESULT 12
US-10-168-185-2
Sequence 2, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Miesbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jürgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-185-2
```

```
Query Match      67.8%  Score 40; DB 14; Length 9;
Best Local Similarity 88.9%  Pred. No. 1e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AVSEIQLMH 9
      : |||||:|
Db      1 SVSEIQLMH 9
```

```
RESULT 13
US-10-192-673-8
Sequence 8, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
Parathyroid Hormone (PTH) and Parathyroid
```

```
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
FILE REFERENCE: 0609.4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-10-192-673-8
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Query Match      55.9%  Score 33; DB 14; Length 9;
Best Local Similarity 77.8%  Pred. No. 1e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 AVSEIQLMH 9
      : |||||:|
Db      1 AVSEIQLMH 9
```

```
RESULT 14
US-10-168-185-3
Sequence 3, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Miesbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jürgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-185-3
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```
Query Match      54.2%  Score 32; DB 14; Length 8;
Best Local Similarity 87.5%  Pred. No. 1e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AVSEIQLMH 8
      : |||||:
Db      1 SVSEIQLMH 8
```

```
RESULT 15
US-10-192-673-10
Sequence 10, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
```

Tue May 18 12:03:07 2004

us-09-730-174a-5.closed.rapb

Page 5

;
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)
; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
; US-10-192-673-10

Query Match 50.8%; Score 30; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06; 1; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9
: ||| ||:
Db 1 SVSEHQLH 9

Search completed: May 18, 2004, 10:21:00
Job time : 34.25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:58:45 ; Search time 12.75 Seconds
(without alignments)
48.589 Million cell updates/sec

Title: US-09-730-174A-5
Perfect score: 59
Sequence: 1 AVESEIQLMHLNG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 53 | 89.8 | 12 | 4 | US-09-442-989-31 |
| 2 | 46 | 78.0 | 10 | 3 | US-08-817-547A-1 |
| 3 | 43 | 72.9 | 9 | 4 | US-09-421-379-6 |
| 4 | 40 | 67.8 | 9 | 3 | US-08-817-547A-2 |
| 5 | 40 | 67.8 | 9 | 4 | US-09-421-379-7 |
| 6 | 35 | 59.3 | 11 | 6 | 5460978-3 |
| 7 | 33 | 55.9 | 9 | 4 | US-09-421-379-8 |
| 8 | 32 | 54.2 | 8 | 3 | US-08-817-547A-3 |
| 9 | 30 | 50.8 | 9 | 4 | US-09-421-379-10 |
| 10 | 27 | 45.8 | 7 | 3 | US-08-817-547A-4 |
| 11 | 25 | 42.4 | 10 | 2 | US-08-428-257A-14 |
| 12 | 25 | 42.4 | 11 | 3 | US-08-802-981-124 |
| 13 | 24 | 40.7 | 5 | 2 | US-08-177-109A-56 |
| 14 | 24 | 40.7 | 5 | 2 | US-08-687-706-56 |
| 15 | 24 | 40.7 | 5 | 3 | US-08-817-547A-17 |
| 16 | 24 | 40.7 | 6 | 3 | US-08-817-547A-16 |
| 17 | 24 | 40.7 | 7 | 3 | US-08-817-547A-15 |
| 18 | 24 | 40.7 | 8 | 2 | US-08-748-021-64 |
| 19 | 24 | 40.7 | 8 | 3 | US-08-817-547A-14 |
| 20 | 24 | 40.7 | 8 | 3 | US-08-974-297-64 |
| 21 | 24 | 40.7 | 9 | 3 | US-08-817-547A-13 |
| 22 | 24 | 40.7 | 10 | 3 | US-08-817-547A-7 |
| 23 | 24 | 40.7 | 11 | 2 | US-08-726-464B-13 |
| 24 | 24 | 40.7 | 11 | 4 | US-09-428-082B-41 |
| 25 | 23 | 39.0 | 6 | 3 | US-08-817-547A-5 |
| 26 | 23 | 39.0 | 7 | 4 | US-09-316-093-12 |
| 27 | 23 | 39.0 | 7 | 4 | US-09-557-465D-12 |

| | | | | | | |
|----|----|------|----|---|--------------------|-------------------|
| 28 | 23 | 39.0 | 10 | 3 | US-08-396-385-6 | Sequence 6, Appl |
| 29 | 23 | 39.0 | 10 | 4 | US-09-287-221-6 | Sequence 6, Appl |
| 30 | 23 | 39.0 | 12 | 2 | US-08-140-137A-42 | Sequence 42, Appl |
| 31 | 23 | 39.0 | 12 | 4 | US-08-474-349A-271 | Sequence 271, App |
| 32 | 22 | 37.3 | 8 | 3 | US-08-160-604-74 | Sequence 74, Appl |
| 33 | 22 | 37.3 | 8 | 3 | US-08-160-604-75 | Sequence 75, Appl |
| 34 | 22 | 37.3 | 8 | 4 | US-09-296-089-10 | Sequence 10, Appl |
| 35 | 22 | 37.3 | 8 | 4 | US-09-551-976-10 | Sequence 10, Appl |
| 36 | 22 | 37.3 | 9 | 4 | US-08-492-543-177 | Sequence 177, App |
| 37 | 22 | 37.3 | 11 | 3 | US-08-652-877-71 | Sequence 71, Appl |
| 38 | 22 | 37.3 | 11 | 3 | US-08-160-604-73 | Sequence 73, Appl |
| 39 | 22 | 37.3 | 11 | 3 | US-08-476-515A-71 | Sequence 71, Appl |
| 40 | 22 | 37.3 | 11 | 4 | US-09-296-089-27 | Sequence 27, Appl |
| 41 | 22 | 37.3 | 11 | 4 | US-08-475-955-56 | Sequence 56, Appl |
| 42 | 22 | 37.3 | 11 | 4 | US-09-551-976-27 | Sequence 27, Appl |
| 43 | 22 | 37.3 | 12 | 4 | US-09-690-454-89 | Sequence 89, Appl |
| 44 | 22 | 37.3 | 12 | 4 | US-09-591-694-41 | Sequence 41, Appl |
| 45 | 21 | 35.6 | 6 | 2 | US-08-621-803-184 | Sequence 184, App |

ALIGNMENTS

RESULT 1
US-09-442-989-31
Sequence 31, Application US/09442989
Patent No. 6565993
GENERAL INFORMATION:
APPLICANT: Sledgeki, James J.
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
FILE REFERENCE: A3113B-US
CURRENT APPLICATION NUMBER: US/09/442,989
CURRENT FILING DATE: 1999-11-18
EARLIER APPLICATION NUMBER: 60/081,897
EARLIER FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)
OTHER INFORMATION: FMOC-Ala
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (3)
OTHER INFORMATION: Ser(OtBu)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (4)
OTHER INFORMATION: Glu(OtBu)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (5)
OTHER INFORMATION: Glu(Ttc)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (9)
OTHER INFORMATION: His(Ttc)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (10)
OTHER INFORMATION: Asn(Ttc)
FEATURE:
NAME/KEY: MOD RES
LOCATION: (8)
OTHER INFORMATION: Nle
US-09-442-989-31

Query Match 89.8%; Score 53; DB 4; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQLMNLS 12
DB 1 AVSEIQLMNLS 12

RESULT 2
US-08-817-547A-1
Sequence 1, Application US/08817547A

PATENT No. 6030790
GENERAL INFORMATION:
APPLICANT: Ademann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-817-547A-1

Query Match 78.0%; Score 46; DB 3; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.019;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMN 10
DB 1 AVSEIQLMN 10

RESULT 3
US-09-421-379-6
Sequence 6, Application US/09421379
PATENT No. 6495662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Krenenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald

TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)
FILE REFERENCE: 0609.4570001, 379
CURRENT APPLICATION NUMBER: US/09/421,379
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 6
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-6

Query Match 72.9%; Score 43; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9
DB 1 AVSEIQLMH 9

RESULT 4
US-08-817-547A-2
Sequence 2, Application US/08817547A
PATENT No. 6030790
GENERAL INFORMATION:
APPLICANT: Ademann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-817-547A-2

Query Match 67.8%; Score 40; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9
Db 1 AVSEIQLMH 9

RESULT 5
US-09-421-379-7
Sequence 7, Application US/09421379
Patent No. 6495662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
FILE REFERENCE: 0609.4570001
CURRENT APPLICATION NUMBER: US/09/421,379
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 7
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-7

Query Match 67.8%; Score 40; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9
Db 1 AVSEIQLMH 9

RESULT 6
5460978-3
Patent No. 5460978
APPLICANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,
BRUCE E.; WETTENHAL, RICHARD E.H.
TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL
HYPERCALCEMIA OF MALIGNANCY-PTHrP
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/715,280
FILING DATE: 14-JUN-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 199,235
FILING DATE: 09-MAY-1988
APPLICATION NUMBER:
FILING DATE:
SEQ ID NO: 3
LENGTH: 11
5460978-3

Query Match 59.3%; Score 35; DB 6; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 10
|||||

Db 1 AVSEHQLH 10

RESULT 7
US-09-421-379-8
Sequence 8, Application US/09421379
Patent No. 6495662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
FILE REFERENCE: 0609.4570001
CURRENT APPLICATION NUMBER: US/09/421,379
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-8

Query Match 55.3%; Score 33; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9
Db 1 AVSEHQLH 9

RESULT 8
US-08-817-547A-3
Sequence 3, Application US/08817547A
Patent No. 6030790
GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magelstein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: no
ANTI-SENSE: no
US-08-817-547A-3

Query Match 54.2%; Score 32; DB 3; Length 8;
Best Local Similarity 87.5%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLM 8
Db 1 SVSEIQLM 8

RESULT 9
US-09-421-379-10
Sequence 10, Application US/09421379
Patent No. 6495662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kromberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
FILE REFERENCE: 0609 4570001
CURRENT APPLICATION NUMBER: US/09/421.379
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-10

Query Match 50.8%; Score 30; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQLM 9
Db 1 SVSEIQLM 9

RESULT 10
US-08-817-547A-4
Sequence 4, Application US/08817547A
Patent No. 6030790
GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Maggeln, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta

STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: no
ANTI-SENSE: no
US-08-817-547A-4

Query Match 45.8%; Score 27; DB 3; Length 7;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQ 7
Db 1 SVSEIQ 7

RESULT 11
US-08-428-257A-14
Sequence 14, Application US/08428257A
Patent No. 5885808
GENERAL INFORMATION:
APPLICANT: Spooner, Robert A.
APPLICANT: Epenetos, A.A.
TITLE OF INVENTION: Compounds to target cells
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EFO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,257A
FILING DATE: 07/05/95
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-257A-14

Query Match 42.4%; Score 25; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 VSEIOL 7
DB 4 VSEVOL 9

RESULT 12
US-08-802-981-124
; Sequence 124, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /Product= "A1b"
; US-08-802-981-124

Query Match 42.4%; Score 25; DB 3; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 OLHN 10
DB 5 OLHN 9

RESULT 13
US-08-177-109A-56
; Sequence 56, Application US/08177109A
; Patent No. 569645
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/177,109A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.

Query Match 40.7%; Score 24; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 8 MENLG 12
DB 1 LHMWG 5

RESULT 14
US-08-687-706-56
; Sequence 56, Application US/08687706
; Patent No. 592892
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,706
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/177,109
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.

Tue May 18 12:03:07 2004

us-09-730-174a-5.closed.rat

Page 6

REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 107 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
-HYPOTHETICAL: NO
US-08-687-706-56

Query Match 40.7%; Score 24; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 8 HNLG 12
DB 1 HNLG 5

RESULT 15
US-08-817-547A-17
Sequence 17, Application US/08817547A
Patent No. 6030790
GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-817-547A-17

Query Match 40.7%; Score 24; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 9 HNLG 12
DB 1 HNLG 4

Search completed: May 18, 2004, 10:06:44
Job time : 12.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:56:10 ; Search time 10.25 Seconds
(without alignments)
112.614 Million cell updates/sec

Title: US-09-730-174a-6
Perfect score: 61
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR 78:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------|
| 1 | 20 | 32.8 | 10 | 2 | S28055 cytochrome b559 co |
| 2 | 20 | 32.8 | 12 | 2 | PH1187 T-cell receptor al |
| 3 | 18 | 29.5 | 7 | 2 | A58718 carnosin u49 - Ca |
| 4 | 18 | 29.5 | 9 | 2 | S78420 ribosomal protein |
| 5 | 18 | 29.5 | 10 | 2 | A60589 sperm-activating p |
| 6 | 18 | 29.5 | 12 | 2 | PH1190 T-cell receptor al |
| 7 | 17 | 27.9 | 8 | 2 | A05169 neuropeptide M-I - |
| 8 | 17 | 27.9 | 10 | 2 | A37268 Ig heavy chain C r |
| 9 | 17 | 27.9 | 12 | 1 | A43975 locustamytroptin - |
| 10 | 17 | 27.9 | 12 | 2 | S21205 Ig heavy chain V r |
| 11 | 17 | 27.9 | 12 | 2 | PH1189 T-cell receptor al |
| 12 | 16 | 26.2 | 7 | 2 | A46868 alpha-myosin heavy |
| 13 | 16 | 26.2 | 10 | 2 | UC1416 hypertrichalosemic |
| 14 | 16 | 26.2 | 10 | 2 | S09138 hypertrichalosemic |
| 15 | 16 | 26.2 | 11 | 2 | A32428 amine oxidase (cop |
| 16 | 15 | 24.6 | 9 | 2 | S29735 polyphosphate-gluc |
| 17 | 15 | 24.6 | 9 | 2 | PT0231 Ig heavy chain CDR |
| 18 | 15 | 24.6 | 9 | 2 | A56029 N-methylpurine DNA |
| 19 | 15 | 24.6 | 10 | 2 | S33844 alpha-2-macroglobu |
| 20 | 15 | 24.6 | 10 | 2 | S38304 lectin GNL1 alpha |
| 21 | 15 | 24.6 | 10 | 2 | E49033 T-cell receptor ga |
| 22 | 15 | 24.6 | 11 | 2 | A38841 rhodopsin homolog |
| 23 | 15 | 24.6 | 12 | 2 | A55837 5-aminimidazole r |
| 24 | 15 | 24.6 | 12 | 2 | PH1174 T-cell receptor al |
| 25 | 15 | 24.6 | 12 | 2 | SM1737 T-cell receptor be |
| 26 | 14 | 23.0 | 7 | 2 | A57779 neuropeptide Antho |
| 27 | 14 | 23.0 | 4 | 2 | S78024 ribosomal protein |
| 28 | 14 | 23.0 | 8 | 2 | S08995 hypertrichalosemic |
| 29 | 14 | 23.0 | 8 | 2 | A49823 adipokinetic hormo |

| | | | | | |
|----|----|------|----|---|---------------------------|
| 30 | 14 | 23.0 | 8 | 2 | A44960 neuropeptide led-C |
| 31 | 14 | 23.0 | 9 | 2 | PM0002 chlorophyll a/b-bi |
| 32 | 14 | 23.0 | 9 | 2 | PT0238 Ig heavy chain CRD |
| 33 | 14 | 23.0 | 10 | 1 | SPEGNK neuromedin K - p19 |
| 34 | 14 | 23.0 | 10 | 2 | S27873 hypothetical prote |
| 35 | 14 | 23.0 | 10 | 2 | C61033 ranatachykinin C - |
| 36 | 14 | 23.0 | 10 | 2 | B46453 e antigen p20e pre |
| 37 | 14 | 23.0 | 10 | 2 | C44787 calliFERamide 12 |
| 38 | 14 | 23.0 | 11 | 2 | B41835 translation elonga |
| 39 | 14 | 23.0 | 11 | 2 | S19301 endo-1,4-beta-xyla |
| 40 | 14 | 23.0 | 11 | 2 | PA0028 protein QA300042 - |
| 41 | 14 | 23.0 | 11 | 2 | S60354 retinal oxidase - |
| 42 | 14 | 23.0 | 11 | 2 | S51436 beta-D-galactosida |
| 43 | 14 | 23.0 | 12 | 2 | S25485 transcription fact |
| 44 | 14 | 23.0 | 12 | 2 | S71034 potB protein - Sal |
| 45 | 14 | 23.0 | 12 | 2 | PH1175 T-cell receptor al |

ALIGNMENTS

RESULT 1

S28055 cytochrome b559 component psbf - pepper chloroplast (fragment)
C1Species: chloroplast Capsicum annuum (pepper)
C1Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jun-1999
C1Accession: S28055
R1Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.
Plant Mol. Biol. 20, 1185-1188, 1992
A1Title: The psbL gene from bell pepper (Capsicum annuum): plaetid RNA editing also occu
A1Reference number: S28055; MUID:93092270; PMID:1463853
A1Accession: S28055
A1Molecule type: DNA
A1Residues: 1-10 <KUN>
A1Cross-References: EMBL:X65570; NID:G14344; P1DN:CAA46539.1; P1D:G415734
C1Genetics:
A1Gene: psbf
A1Genome: chloroplast
C1Superfamily: cytochrome b559 component F
C1Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match 32.8%; Score 20; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 7.4e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFM 8
DB 1 SISAMQFI 8

RESULT 2

PH1187 T-cell receptor alpha chain V region (Cw3/1F11) - human (fragment)
C1Species: Homo sapiens (man)
C1Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C1Accession: PH1187
R1Casanova, J.V.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wic
J. Exp. Med. 176, 439-447, 1992
A1Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A1Reference number: S26512; MUID:92364546; PMID:1180061
A1Accession: PH1187
A1Status: preliminary
A1Molecule type: mRNA
A1Residues: 1-12 <CAS>

Query Match 32.8%; Score 20; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIQFM 7
DB 2 AVSEIQFM 8

RESULT 3

AS8718
carnocin U149 - Carnobacterium sp. (fragment)

C/Species: Carnobacterium sp.
C/Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998

C/Accession: A58718

R/Scifield, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.

Appl. Environ. Microbiol. 58, 1417-1422, 1992

A/Title: Purification and characterization of a new bacteriocin isolated from a Carnobac

A/Reference number: A58718; MUID:92321768; PMID:1622206

A/Accession: A58718

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-7 <STO>

C/Keywords: antibiotic; lanthionine

Query Match 29.5%; Score 18; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Gaps 0;

Matches 4; Conservative 0; Indels 0; Gaps 0;

QY 3 SEIQ 6

Db 2 SEIQ 5

RESULT 4

S78420
ribosomal protein R141, mitochondrial [validated] - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)
C/Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000

C/Accession: S78420

R/Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998

A/Reference number: S78411

A/Accession: S78420

A/Molecule type: protein

A/Residues: 1-9 <COL>

A/Note: the protein is designated as mitochondrial ribosomal protein L41

C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 29.5%; Score 18; DB 2; Length 9;

Best Local Similarity 75.0%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNIG 12

Db 5 HRLG 8

RESULT 5

A60589

sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchi

C/Species: Heterocentrotus mamillatus

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000

C/Accession: A60589

R/Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi, Biochem. Physiol. B 94, 739-751, 1989

A/Title: A halogenated amino acid-containing sperm activating peptide and its related pe

ctus nuda, Echinomera matthei and Heterocentrotus mamillatus.

A/Reference number: A60527

A/Accession: A60589

A/Molecule type: protein

A/Residues: 1-10 <YOS>

C/Superfamily: unassigned animal peptides

Query Match 29.5%; Score 18; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 1.8e+03; Mismatches 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNIG 12

Db 2 YNLG 5

RESULT 6

PH1190
T-cell receptor alpha chain V region (Cw3/10.1) - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C/Accession: PH1190

R/Cananova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A/Reference number: S26512; MUID:92364546; PMID:1380061

A/Accession: PH1190

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-12 <CAS>

Query Match 29.5%; Score 18; DB 2; Length 12;

Best Local Similarity 71.4%; Pred. No. 2.3e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIQ 7

Db 2 AVSEHG 8

RESULT 7

A05169
neuropeptide M-I - American cockroach

C/Species: Periplaneta americana (American cockroach)
C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993

C/Accession: A05169

R/Wiltgen, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L

Biochem. Biophys. Res. Commun. 124, 350-358, 1984

A/Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mas

A/Reference number: A90118; MUID:85046530; PMID:6548628

A/Accession: A05169

A/Molecule type: protein

A/Residues: 1-8 <MT>

C/Keywords: neuropeptide

Query Match 27.9%; Score 17; DB 2; Length 8;

Best Local Similarity 42.9%; Pred. No. 2.8e+05; Mismatches 3; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 EIOPFHN 10

Db 1 EVNFSFN 7

RESULT 8

A37268

Ig heavy chain C region (129) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998

C/Accession: A37268

R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A/Title: Heavy and light chain variable region sequences and antibody properties of anti

A/Reference number: A38740; MUID:91177923; PMID:1706720

A/Accession: A37268

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-10 <RUF>

Query Match 27.9%; Score 17; DB 2; Length 10;

Best Local Similarity 44.4%; Pred. No. 2.9e+03; Mismatches 4; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIOPFHNIG 12

Db 1 ESQSPFNVG 9

RESULT 9

A43975
 locustamytropin - migratory locust
 N:Alternate names: Lom-MT
 C:Species: Locusta migratoria (migratory locust)
 C>Date: 11-Feb-1993 #sequence_revision 02-Jun-1994 #text_change 08-Dec-1995
 C:Accession: A43975
 R:Schroofs, L.; Holman, G.M.; Hayes, T.K.; Tips, A.; Nachman, R.J.; Vandessande, F.; De Le Peetres 11, 427-433, 1990
 A:Title: Isolation, identification and synthesis of locustamytropin (Lom-MT), a novel h A:Reference number: A43975; PMID:1974346
 A:Accession: A43975
 A:Molecule type: protein
 A:Residues: 1-12 <SCH>
 A>Note: the amino end of this peptide is not blocked
 A>Note: Synthetic locustamytropin mimics natural locustamytropin only in the amidated C:Comment: This peptide was shown to stimulate visceral muscle contractions in locust ov C:Superfamily: Pyrokinin
 C:Keywords: amidated carboxyl end; neuropeptide
 F:12/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 27.9%; Score 17; DB 1; Length 12;
 Best Local Similarity 45.8%; Pred. No. 3.5e+03;
 Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AVSEIQFMNLT 11
 Db 2 AVPAQFSPRL 12

RESULT 10

S21205
 Ig heavy chain V region - human
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
 C:Accession: S21205
 R:Makiya, R.; Scigbrand, T.
 Eur. J. Biochem. 205, 341-345, 1992
 A:Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin- A:Reference number: S21205; PMID:92209522; PMID:1555592
 A:Accession: S21205
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <MAK>
 C:Keywords: heterotrimer; immunoglobulin

Query Match 27.9%; Score 17; DB 2; Length 12;
 Best Local Similarity 33.3%; Pred. No. 3.5e+03;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 EIQFMNLTG 12
 Db 1 EVQLVESGG 9

RESULT 11

PH1189
 T-cell receptor alpha chain V region (Cw3/2C3) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: PH1189
 R:Casanova, J.L.; Gerotini, J.C.; Matches, M.; Necker, A.; Gournier, H.; Barra, C.; Wid J. Exp. Med. 176, 439-447, 1992
 A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor A:Reference number: S26512; PMID:92364546; PMID:1380061
 A:Accession: PH1189
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-12 <CAS>

Query Match 27.9%; Score 17; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSE 4
 Db 2 AVSE 5

RESULT 12

146868
 alpha-myosin heavy chain - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
 C:Accession: 146868
 R:Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H. Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
 A:Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula A:Reference number: 146868; PMID:84221901; PMID:6528491
 A:Accession: 146868
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-7 <FRI>
 A:Cross-references: GB:K01698; NID:G165538; PIDN:AAA31415.1; PID:G165539

Query Match 26.3%; Score 16; DB 2; Length 7;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QFMHN 10
 Db 1 QFMND 5

RESULT 13

JC1416
 hypertrehalosemic hormone I - stick insect (Carausius morosus)
 N:Alternate names: neuropeptide Cam-HrTH-I
 N:Contains: hypertrehalosemic factor II
 C:Species: Carausius morosus
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: JC1416; S07157
 R:Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L. Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992
 A:Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick in A:Reference number: JC1416; PMID:93129186; PMID:1482345
 A:Accession: JC1416
 A:Molecule type: protein
 A:Residues: 1-10 <GAE1>
 R:Gaede, G.; Rinehart, K.L. Biol. Chem. Hoppe-Seyler 368, 67-75, 1997
 A:Title: Primary structure of the hypertrehalosemic factor II from the corpus cardiacum A:Reference number: S07157; PMID:87157103; PMID:3828078
 A:Accession: S07157
 A:Molecule type: protein
 A:Residues: 1-2 <GAE2>
 C:Comment: Hypertrehalosemic factor II lacks the tryptophan modification. C:Comment: This peptide raises hemolymph levels of trehalose in the cockroach periplanet C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic ac F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
 F:8/Binding site: carbonyl group (Tyr) (covalent) #status experimental
 F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 26.2%; Score 16; DB 2; Length 10;
 Best Local Similarity 33.3%; Pred. No. 4.5e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMNLTG 12
 Db 1 QLTFTPMWG 9

RESULT 14

S09138

hypertrehalosemic hormone II - stick insect (Extratosoma tiaratum)
 N;Alternate names: Cam-HrTH-II
 C;Species: Extratosoma tiaratum
 C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
 C;Accession: S09138
 R;Gaede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
 A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extratosoma tiaratum assigned by tandem fast atom bombardment
 A;Reference number: S08995; MUID:90253659; PMID:2340112
 A;Accession: S09138
 A;Molecule type: protein
 A;Residues: 1-10 <GAE>
 A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 26.2%; Score 16; DB 2; Length 10;
 Best Local Similarity 33.3%; Pred. No. 4.5e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 4 EIQPMNNG 12
 ::|
 Db 1 QLTFTPNWG 9

RESULT 15

A32428
 A;Name: amine oxidase (copper-containing) (EC 1.4.3.6) - pig (fragment)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 06-Sep-1996
 C;Accession: A32428
 R;van der Meer, R.A.; van Maassen, P.D.; van Brouwerhaven, J.H.; Duine, J.A.
 Biochem. Biophys. Res. Commun. 159, 726-733, 1989
 A;Title: Primary structure of a pyrroloquinoline quinone (PQQ) containing peptide isolated from the pig
 A;Reference number: A32428; MUID:89193662; PMID:2539124
 A;Accession: A32428
 A;Molecule type: protein
 A;Residues: 1-7, 'K', '9-11 <VAN>
 A;Note: the modified residue thought by the authors to be pyrroloquinoline quinone covalently bound to the protein
 C;Keywords: oxidoreductase; quinoprotein; topaquinone
 F;8/Modified site: topaquinone (Tyr) #status predicted

Query Match 26.2%; Score 16; DB 2; Length 11;
 Best Local Similarity 37.5%; Pred. No. 5e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 SEIOFMHN 10
 |::|
 Db 2 SDAVFTVN 9

Search completed: May 18, 2004, 10:05:41
 Job time : 10.25 secs

Tue May 18 12:03:12 2004

us-09-730-174a-6.closed.rsp

Page 1

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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:43:45 ; Search time 6.75 Seconds

(without alignments)
92.569 Million cell updates/sec

Title: US-09-730-174A-6

Perfect score: 61

Sequence: 1 ANSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt 42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | ID | Description |
|------------|-------|-------|--------------|----|-------------|
| 1 | 20 | 32.8 | 10 | 1 | PSBF_CAPAN |
| 2 | 18 | 29.5 | 7 | 1 | LANC_CARUT |
| 3 | 18 | 29.5 | 10 | 1 | HTF1_ROMMI |
| 4 | 17 | 27.9 | 12 | 1 | LMT1_LOCM1 |
| 5 | 16 | 26.2 | 8 | 1 | ALP6_CYDPO |
| 6 | 16 | 26.2 | 10 | 1 | HTF2_CARMO |
| 7 | 15 | 24.6 | 5 | 1 | EIO3_LITRU |
| 8 | 15 | 24.6 | 8 | 1 | FUS8_FUSSO |
| 9 | 15 | 24.6 | 11 | 1 | EFG_CLOPA |
| 10 | 15 | 24.6 | 11 | 1 | NUHM_CANPA |
| 11 | 14 | 23.0 | 4 | 1 | FLRN_ATEL |
| 12 | 14 | 23.0 | 7 | 1 | ALP7_CYDPO |
| 13 | 14 | 23.0 | 7 | 1 | TY51_LITRU |
| 14 | 14 | 23.0 | 8 | 1 | AL18_CARPA |
| 15 | 14 | 23.0 | 8 | 1 | AL11_CYDPO |
| 16 | 14 | 23.0 | 8 | 1 | HTF1_PEPAM |
| 17 | 14 | 23.0 | 9 | 1 | FAR8_MACRS |
| 18 | 14 | 23.0 | 9 | 1 | UFO2_MOUSE |
| 19 | 14 | 23.0 | 10 | 1 | AL19_CARMA |
| 20 | 14 | 23.0 | 10 | 1 | FAR2_PENMO |
| 21 | 14 | 23.0 | 10 | 1 | FARC_CALVO |
| 22 | 14 | 23.0 | 10 | 1 | TRNC_PANCA |
| 23 | 14 | 23.0 | 10 | 1 | TRNC_PIG |
| 24 | 14 | 23.0 | 11 | 1 | ASL1_BACSE |
| 25 | 14 | 23.0 | 12 | 1 | PORD_METTM |
| 26 | 14 | 23.0 | 12 | 1 | RS19_TOBBP |
| 27 | 13 | 21.3 | 6 | 1 | TRP1_PSEPU |
| 28 | 13 | 21.3 | 8 | 1 | HTF_TENMO |
| 29 | 13 | 21.3 | 8 | 1 | LCK4_LEUVA |
| 30 | 13 | 21.3 | 8 | 1 | LCK6_LEUVA |
| 31 | 13 | 21.3 | 9 | 1 | CONO_CONGE |
| 32 | 13 | 21.3 | 9 | 1 | MOSH_CLYYA |
| 33 | 13 | 21.3 | 9 | 1 | OXYT_EISFO |

| | | | | | |
|----|----|------|----|---|------------|
| 34 | 13 | 21.3 | 9 | 1 | PPK1_PPRAM |
| 35 | 13 | 21.3 | 11 | 1 | ASL2_BACSE |
| 36 | 13 | 21.3 | 11 | 1 | COR2_PPRAM |
| 37 | 13 | 21.3 | 11 | 1 | CS15_BACSU |
| 38 | 13 | 21.3 | 11 | 1 | FKV1_PPRAM |
| 39 | 13 | 21.3 | 11 | 1 | OZOA_COMTE |
| 40 | 13 | 21.3 | 12 | 1 | UKA2_HUMAN |
| 41 | 12 | 19.7 | 5 | 1 | RE21_LITRU |
| 42 | 12 | 19.7 | 5 | 1 | RE21_LITRU |
| 43 | 12 | 19.7 | 8 | 1 | ANG2_BOTUA |
| 44 | 12 | 19.7 | 8 | 1 | HTP2_PPRAM |
| 45 | 12 | 19.7 | 9 | 1 | FIBB_ERIYA |

ALIGNMENTS

RESULT 1

PSBF_CAPAN STANDARD; PRT; 10 AA.

AC Q03367;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI)
DE (Fragment).
OS PSBF.
GN Capsicum annuum (Bell pepper).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Capsicum.
CX NCBI_TaxID=4072;
RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lamuyo; TISSUE=fruit, and leaf;
RX MEDLINE=93099270; PubMed=1463853;
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;
RT "the psbI gene from bell pepper (Capsicum annuum): plastid RNA
editing also occurs in non-photosynthetic chromoplasts.";
RL Plant Mol. Biol. 20:1185-1188(1992).
CC -!- FUNCTION: This b-type cytochrome is tightly associated with the
CC reaction center of photosystem II and possibly is part of the
CC water-oxidation complex.
CC -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC -!- SIMILARITY: Belongs to the psbI / psbF family.

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CC
CC EMBL: X65570; CAA46539.1; -
DR HAMAP: MF 00643; -!-
DR HAMAP: MF 00643; -!-
DR InterPro: IPR006216; Cyt b559.
DR PROSITE: PS00537; CYTOCHROME B559; PARTIAL.
KM Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
KW NON TER
FT DOMAIN
FT TRANSMEM
FT NON TER
SQ SEQUENCE 10 AA; 1180 MW; 817D0F59D6D59DC5 CRC64;

Query Match 32.8%; Score 20; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 4.8e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 ANSEIQFM 8
DB 1 SISAMQFI 8

```

RESULT 2
ID LANC_CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin U149 (Fragment).
OS Carnobacterium sp. (strain U149).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -1- FUNCTION: Lantionine-containing peptide antibiotic (lantibiotic).
CC Active on Gram-positive bacteria.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON TER
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 29.5%; Score 18; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEQ 6
Db 2 SEQ 5

RESULT 3
HTFL_ROMMI
ID HTFL_ROMMI STANDARD; PRT; 10 AA.
AC P1810;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RO I (Hypertrehalosemic factor).
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caellifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
NCBI_TaxID=7007;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
DE MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1986).
CC -1- FUNCTION: Hypertrehalosemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC InterPro: IPR002047; AKH.
DR PROSITE; PS00255; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;

Query Match 29.5%; Score 18; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 4 EIQEWANIG 12
Db 1 QNFTFPMWG 9

RESULT 4
ID LMT1_LOCMI STANDARD; PRT; 12 AA.
AC P22395;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE Locustamyotropin 1 (LOM-MT-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caellifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
DE MEDLINE=90341077; PubMed=1974346;
RA Schoofs L., Holman G.W., Hayes T.K., Tips A., Nachman R.J.,
RA Vandensande F., de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin
RT (LOM-MT), a novel biologically active insect peptide.";
RL Peptides 11:427-433(1990).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SIMILARITY: Belongs to the pyrokinin family.
CC PIR; A43975; A43975.
DR InterPro; IPR001484; PYROKININ.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 12 AMIDATION.
SQ SEQUENCE 12 AA; 1213 MW; D766C92722D6DD CRC64;

Query Match 27.9%; Score 17; DB 1; Length 12;
Best Local Similarity 45.5%; Pred. No. 2.3e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AVSEIQFHNH 11
Db 2 AVPAQFSPRL 12

RESULT 5
ID ALLE_CYPDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydistastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RX TISSUE=Larva;
DE MEDLINE=98054539; PubMed=9392829;
RA Duvé H., Johnsen A.H., Maestre J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

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ID EFG CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
NCBI_TaxID=1501;
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=WS;
RX MEDLINE=98291870; PubMed=9629918;
RA Flanagan R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum WS.";
RL Electrophoresis 19:802-806(1998).
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of
the nascent protein chain from the A-site to the P-site of the
ribosome.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC InterPro: IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACITOR_GTP, PARTIAL.
KM Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C3B17 CRC64;
QY 5 IQFMHNG 12
Db 4 LKFNQIG 11
RESULT 10
ID NUHM CANFA STANDARD; PRT; 11 AA.
AC P49820;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Fragment).
GN NDUFV2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn W.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
FRAGMENT OF THE ENZYME.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -1- COFACTOR: Binds 1 2Fe-2S cluster (potential).
CC -1- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC -1- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
mitochondrial inner membrane.
CC -1- SIMILARITY: Belongs to the complex I 24 kDa subunit family.

DR HSC-2DPAGE; P49820; DOG.
DR InterPro: IPR002023; Cmplx1_24kDa.
DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
KM Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
FT NON_TER 11
SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;
QY 7 FMHN 10
Db 1 FLRN 4
RESULT 11
ID FLRN ANTEL STANDARD; PRT; 4 AA.
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nyantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheid R.K., Nohacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenylacetyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron specific.
CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAE.
DR PIR; A35779; A35779.
KM Neuropeptide; Amidation.
FT MOD_RES 1
FT MOD_RES 4
FT MOD_RES 4
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;
QY 7 FMHN 10
Db 1 FLRN 4
RESULT 12
ID ALL7 CYDPO STANDARD; PRT; 7 AA.
AC P82158;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydia pomonella (Codling moth).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditylsia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;

RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Duvé H., East P.D., Thorpe A.,
 RT "Lepidopteran peptides of the allatostatin superfamily."
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Amidation.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 873 MW; 672879CAB569350 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 7;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 HNLG 12
 DB 2 WYDFG 6

RESULT 13
 ID TY51_LITRU STANDARD; PRT; 7 AA.
 AC P82065;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Trypophyllin 5.1.
 OS Litoria rubella (Desert tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyllidae;
 CC Pelodytidae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinhorn S.T., Wabnitz P.A., Maugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT of evolutionary trends of amphibians."
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -1- MASS SPECTROMETRY: MW=965; METHOD=FAE.
 KW Amphibian defense peptide; Amidation; Neuropeptide;
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 1 7
 FT MOD RES 7 7
 SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 7;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 BIOFMH 9
 DB 1 QIPWFH 6

RESULT 14
 ID AL18_CARMA STANDARD; PRT; 8 AA.
 AC P81821;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinostatin 18.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaro P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas."
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 CC Neuropeptide; Amidation; Multigene family.
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 919 MW; C62879D5B569A5 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 HNLG 12
 DB 3 WYDFG 7

RESULT 15
 ID ALL1_CYPDO STANDARD; PRT; 8 AA.
 AC P82152;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiaastatin 1.
 OS Cydia pomonella (Coddling moth).
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Duvé H., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily."
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 CC Neuropeptide; Amidation.
 FT MOD RES 8
 FT MOD RES 8 8
 SQ SEQUENCE 8 AA; 934 MW; C62879C45B51F775 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12
 DB 4 YNFG 7

Search completed: May 18, 2004, 10:02:34
 Job time : 6.75 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 09:55:20 ; Search time 30.25 Seconds
(without alignments)
125.164 Million cell updates/sec

Title: US-09-730-174A-6
Perfect score: 61
Sequence: 1 AVESEIQFHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_XYTRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 24 | 39.3 | 11 | 13 Q9PS71 | Q9PS71 agkistrodon |
| 2 | 19 | 31.1 | 8 | 6 Q9TT78 | Q9TT78 canis fam1 |
| 3 | 19 | 31.1 | 9 | 12 Q92766 | Q92766 canine dist |
| 4 | 19 | 31.1 | 9 | 12 Q71066 | Q71066 canine dist |
| 5 | 19 | 31.1 | 12 | 13 P82081 | P82081 limnodynast |
| 6 | 18 | 29.5 | 8 | 3 Q13591 | Q13591 saccharomyc |
| 7 | 18 | 29.5 | 12 | 8 Q8M50 | Q8M50 anoda crist |
| 8 | 18 | 29.5 | 12 | 15 Q85631 | Q85631 avian carci |
| 9 | 17 | 27.9 | 11 | 5 Q23876 | Q23876 dicystocell |
| 10 | 17 | 27.9 | 12 | 13 P82085 | P82085 limnodynast |
| 11 | 16 | 26.2 | 7 | 6 Q28742 | Q28742 oryctolagus |
| 12 | 16 | 26.2 | 8 | 3 Q05403 | Q05403 saccharomyc |
| 13 | 16 | 26.2 | 8 | 10 Q40659 | Q40659 oryza sativ |
| 14 | 16 | 26.2 | 8 | 13 P82082 | P82082 limnodynast |
| 15 | 16 | 26.2 | 8 | 13 P82083 | P82083 limnodynast |
| 16 | 16 | 26.2 | 9 | 2 Q44377 | Q44377 aeromonas t |

| | | | | | |
|----|----|------|----|-----------|--------------------|
| 17 | 16 | 26.2 | 9 | 2 Q44468 | Q44468 aeromonas v |
| 18 | 16 | 26.2 | 9 | 2 Q8RXU3 | Q8RXU3 borrelia bu |
| 19 | 16 | 26.2 | 9 | 2 Q43928 | Q43928 aeromonas p |
| 20 | 16 | 26.2 | 9 | 2 Q44001 | Q44001 aeromonas e |
| 21 | 16 | 26.2 | 9 | 10 Q9FX10 | Q9FX10 ilium long |
| 22 | 16 | 26.2 | 10 | 10 P82132 | P82132 spinacia ol |
| 23 | 16 | 26.2 | 10 | 10 P82133 | P82133 spinacia ol |
| 24 | 16 | 26.2 | 11 | 8 Q9GDE8 | Q9GDE8 elaeis guin |
| 25 | 16 | 26.2 | 11 | 10 P82336 | P82336 pisum sativ |
| 26 | 15 | 24.6 | 8 | 4 Q15894 | Q15894 homo sapien |
| 27 | 15 | 24.6 | 8 | 8 Q34909 | Q34909 locusta mig |
| 28 | 15 | 24.6 | 8 | 13 Q90493 | Q90493 eopsaltria |
| 29 | 15 | 24.6 | 9 | 2 Q43960 | Q43960 azotobacter |
| 30 | 15 | 24.6 | 9 | 4 Q15891 | Q15891 homo sapien |
| 31 | 15 | 24.6 | 9 | 10 Q883C6 | Q883C6 glycine max |
| 32 | 15 | 24.6 | 9 | 10 Q9FEC0 | Q9FEC0 hordeum vul |
| 33 | 15 | 24.6 | 10 | 4 Q15342 | Q15342 homo sapien |
| 34 | 15 | 24.6 | 10 | 5 P82222 | P82222 bombyx mori |
| 35 | 15 | 24.6 | 10 | 10 Q8GZC8 | Q8GZC8 hordeum vul |
| 36 | 15 | 24.6 | 11 | 4 Q9C057 | Q9C057 homo sapien |
| 37 | 15 | 24.6 | 11 | 6 Q9BDC8 | Q9BDC8 pongo pygma |
| 38 | 15 | 24.6 | 11 | 6 Q9BD09 | Q9BD09 gorilla gor |
| 39 | 15 | 24.6 | 11 | 6 Q9BD09 | Q9BD09 pan troglod |
| 40 | 15 | 24.6 | 11 | 6 Q9BDC9 | Q9BDC9 pan paniscu |
| 41 | 15 | 24.6 | 12 | 4 Q9UNV5 | Q9UNV5 homo sapien |
| 42 | 14 | 23.0 | 7 | 8 Q9J182 | Q9J182 gnatholebia |
| 43 | 14 | 23.0 | 8 | 2 Q49534 | Q49534 mycoplasma |
| 44 | 14 | 23.0 | 8 | 12 Q84156 | Q84156 orf virus (|
| 45 | 14 | 23.0 | 8 | 13 Q91098 | Q91098 manorina me |

ALIGNMENTS

| | | | | | |
|---|---------|--------------------|------------------------|------------|----|
| RESULT 1 | | | | | |
| Q9PS71 | | PRELIMINARY; | PRT; | 11 AA. | |
| AC Q9PS71 | | | | | |
| DT 01-MAY-2000 (TREMREL. 13, Created) | | | | | |
| DT 01-MAY-2000 (TREMREL. 13, Last sequence update) | | | | | |
| DT 01-JUN-2002 (TREMREL. 21, Last annotation update) | | | | | |
| DE Fibrinolytic metalloproteinase (Fragment). | | | | | |
| OS Agkistrodon contortrix. | | | | | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea; | | | | | |
| OC Viperidae; Crotalinae; Agkistrodon. | | | | | |
| OX NCBI_Taxid=8720; | | | | | |
| RN [1] | | | | | |
| RP SEQUENCE. | | | | | |
| RX MEDLINE=91378546; Pubmed=1898066; | | | | | |
| RA Guan A.L., Retzius A.D., Henderson G.N., Markland F.S.Jr.; | | | | | |
| RT "Purification and characterization of a fibrinolytic enzyme from venom | | | | | |
| RT of the southern copperhead snake (Agkistrodon contortrix). | | | | | |
| RT contortrix); " | | | | | |
| RL Arch. Biochem. Biophys. 289:197-207(1991). | | | | | |
| FT NON TER | 11 | 11 | | | |
| FT SEQUENCE | 11 AA; | 1209 MW; | 7CA02D1D4EB772B CRC64; | | |
| Query Match | 39.3%; | Score 24; | DB 13; | Length 11; | |
| Best Local Similarity | 100.0%; | Pred. No. 6.3e-02; | | | |
| Matches | 4; | Conservative | 0; | Mismatches | 0; |
| | | | | Indels | 0; |
| | | | | Gaps | 0; |
| QY | 9 | HNLG 12 | | | |
| DB | 7 | HNLG 10 | | | |
| RESULT 2 | | | | | |
| Q9TT78 | | PRELIMINARY; | PRT; | 8 AA. | |
| AC Q9TT78 | | | | | |
| DT 01-MAY-2000 (TREMREL. 13, Created) | | | | | |
| DT 01-MAY-2000 (TREMREL. 13, Last sequence update) | | | | | |

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DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Thymidylate synthase (Fragment).
GN TS
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015404; PubMed=11130975;
RA Brouillette J.A., Andrew J.R., Venta P.J.;
RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
RT method.";
RL Mamm. Genome 11:1079-1086(2000).
DR EMBL; AF202073; AAF20918.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 8 AA; 899 MW; 6731AE059CA867 CRC64;

Query Match 31.1%; Score 19; DB 6; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 FMHNL 11
DB 4 FHRTL 8

RESULT 3
ID 092766 PRELIMINARY; PRT; 9 AA.
AC 092766;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Dog #5526/89;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026237; AAC09167.1; -.
FT NON TER 9
FT NON TER 9
SQ SEQUENCE 9 AA; 1011 MW; F26173276053441 CRC64;

Query Match 31.1%; Score 19; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 10
DB 1 MHN 3

RESULT 4
ID 071066 PRELIMINARY; PRT; 9 AA.
AC 071066;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

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OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Dog #10757/96;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026234; AAC09164.1; -.
FT NON TER 9
FT NON TER 9
SQ SEQUENCE 9 AA; 1124 MW; F29D04576044041 CRC64;

Query Match 31.1%; Score 19; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 10
DB 1 MHN 3

RESULT 5
ID P82081 PRELIMINARY; PRT; 12 AA.
AC P82081;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DYNASTIN 3.
OS Limodactylus terraereginae (Northern banjo frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Nyobatrachidae;
OC Limodactylinae; Limodactylus.
OX NCBI_TaxID=104894;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RX TISSUE=LIVER; GLAND.
RA Rattery W.J., Bristford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT the banjo frogs Limodactylus terraereginae and Limodactylus
RT Limodactylus terraereginae.";
RL Aust. J. Chem. 46:833-842(1993).
CC -1- MASS SPECTROMETRY: MW=1236; METHOD=PAB.
SQ SEQUENCE 12 AA; 1236 MW; 147AA70FD472724 CRC64;

Query Match 31.1%; Score 19; DB 13; Length 12;
Best Local Similarity 60.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 12
DB 7 LNNLG 11

RESULT 6
ID 013591 PRELIMINARY; PRT; 8 AA.
AC 013591;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE ORF YNL337W (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Obermaler B., Piravandi E., Rinke M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

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RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z71612; CA9627.2; -
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 1005 MW; 5CA41E449C9C720 CRC64;

Query Match 29.5%; Score 18; DB 3; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FMEN 10
 DB 4 FMEN 7

RESULT 7
 ID Q8MES0 PRELIMINARY; PRT; 12 AA.
 AC Q8MES0;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Anoda cristata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroids II; Malvales; Malvaceae; Malvoideae; Anoda.
 CX NCBI_TaxID=183227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of nchf and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL: AF384567; AAM50405.1; -
 DR GO: 0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1431 MW; 9A5E59B5452C9CA CRC64;

Query Match 29.5%; Score 18; DB 8; Length 12;
 Best Local Similarity 37.5%; Pred. No. 1.1e+04;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 EIOFMENL 11
 DB 3 EPPFVNNI 10

RESULT 8
 ID Q85631 PRELIMINARY; PRT; 12 AA.
 AC Q85631;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MH2, proviral DNA, myc to 3' LTR (Fragment).
 OS Avian carcinoma virus.
 OC Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.
 CX NCBI_TaxID=11958;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85033920; PubMed=6092695;
 RA Sutcliffe P., Jensen H.W., Bister K., Rapp U.R.;
 RT "3'-terminal region of avian carcinoma virus MH2 shares sequence
 RT elements with avian sarcoma viruses YJ3 and SR-A.";
 RL J. Virol. 52:703-705(1984).
 DR EMBL: K03100; AAA42388.1; -
 FT NON_TER 1

SQ SEQUENCE 12 AA; 1466 MW; 72B4B884F30726DB CRC64;

Query Match 29.5%; Score 18; DB 15; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNL 11
 DB 2 HNL 4

RESULT 9
 ID Q23876 PRELIMINARY; PRT; 11 AA.
 AC Q23876;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE Actin 4.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 CX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=82260445; PubMed=6286214;
 RA McKown M., Firtel R.A.;
 RT "Actin multigene family of Dictyostelium.";
 RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
 DR EMBL: K02957; AAA3150.1; -
 DR EMBL: K02956; AAA3150.1; JOINED.
 SQ SEQUENCE 11 AA; 1205 MW; 72B84C1466C2CAAB CRC64;

Query Match 27.9%; Score 17; DB 5; Length 11;
 Best Local Similarity 28.6%; Pred. No. 1.6e+04;
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 EIOFMEN 10
 DB 5 DVQALNN 11

RESULT 10
 ID P82085 PRELIMINARY; PRT; 12 AA.
 AC P82085;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE DYNASTIN 7.
 OS Limnodynastes salmiani (Salmian's-striped frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Limnodynastinae; Limnodynastes.
 CX NCBI_TaxID=39404;
 RN [1]
 RP SEQUENCE AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structure of the dynastins from
 RT Limnodynastes salmiani and Fletcherin from Limnodynastes fletcheri.";
 RL Aust. J. Chem. 46:1235-1244(1993).
 CC -1- MASS SPECTROMETRY: MW=1114; METHOD=FAE.
 SQ SEQUENCE 12 AA; 1114 MW; 3AB5A976CA72728 CRC64;

Query Match 27.9%; Score 17; DB 13; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.8e+04;
 Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 AVSEIOFMENLG 12
 DB 2 AVSGL-LTNLG 11

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RESULT 11
QY 028742 PRELIMINARY; PRT; 7 AA.
AC Q28742;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
RA Radnawitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01598; AAA31415.1; -.
PIR; I46868; I46868.
FT NON TER 1
SQ SEQUENCE 7 AA; 916 MW; 681B1A1DE9326B0 CRC64;

Query Match 26.2%; Score 16; DB 6; Length 7;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QFMEN 10
DB 1 QFMEN 5
ID Q05403 PRELIMINARY; PRT; 8 AA.
AC Q05403;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE DNA for ORF's from chromosome XV (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FY1679;
RX MEDLINE=96021609; PubMed=8533473;
RA Zunshtein B., Pearson B.M., Kalogetopoulos A., Schweizer M.;
RA "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames.";
RL Yeast 11:975-986(1995).
DR EMBL; X83121; CA58183.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 879 MW; 7B5322DC441E056 CRC64;

Query Match 26.2%; Score 16; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 11
DB 2 MHN 5
ID Q0659 PRELIMINARY; PRT; 8 AA.
AC Q0659;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

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DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Alpha-amylase (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriocaulaceae; Oryzaceae; Oryza.
NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91078641; PubMed=2258052;
RA Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA Rodriguez R.L.;
RT "Expression and secretion of rice alpha-amylase by saccharomycetes
RT cerevisiae.";
RL Gene 94:209-216(1990).
DR EMBL; M62916; AAA33892.1; -.
DR Gramene; Q40659; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;

Query Match 26.2%; Score 16; DB 10; Length 8;
Best Local Similarity 28.6%; Pred. No. 1e+06;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 IOFMEN 11
DB 1 IOFMEN 7
ID P82082 PRELIMINARY; PRT; 8 AA.
AC P82082;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DYNASTIN 4.
OS Limodynastes salmuni (Salmun's-striped frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limodynastinae; Limodynastes.
NCBI_TaxID=39404;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Rafferty M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT Limodynastes salmuni and Fletcherin from Limodynastes fletcheri.";
RL Aust. J. Chem. 46:1235-1244(1993).
CC -1- MASS SPECTROMETRY; MW=772; METHOD=FAE.
SQ SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;

Query Match 26.2%; Score 16; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLG 12
DB 5 NLG 7
ID P82083 PRELIMINARY; PRT; 8 AA.
AC P82083;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE DYNASTIN 5.
OS Limodynastes salmuni (Salmun's-striped frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limodynastinae; Limodynastes.

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OX NCBI_TaxID=39404;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
Limodynastes salmiani and Fletcherin from Limodynastes fletcheri.";
RL Aust. J. Chem. 46:1235-1244(1993).
CC -1- MASS SPECTROMETRY: MW=786; METHOD=PAD
SQ SEQUENCE 8 AA; 786 MW; 7B5877245B05728 CRC64;

Query Match 26.2%; Score 16; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
10 NLG 12
5 NLG 7
Db

Search completed: May 18, 2004, 10:04:48
Job time : 30.25 secs

CC formed from the N-terminus of parathyroid hormone (PTH). Also included
 CC are: (1) a method for producing antibodies useful in the determination of
 CC PTH levels in a biological sample comprising: (a) providing at least one
 CC first peptide antigen comprising a peptide fragment of PTH; (b)
 CC administering the first peptide antigen to a host animal to induce
 CC antibody production; (c) monitoring the antibody titre produced; (d)
 CC isolating antisera produced in the host animal; and (e) selecting
 CC antisera from the isolated antisera produced in the host that is capable
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by
 CC the method; and (3) test kits and analytical procedures used for the
 CC determination of bioactive intact PTH utilising (ab). The method and
 CC compositions of the present invention are useful for determining
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
 CC The antigens, antibodies and methods of the present invention, as
 CC compared to prior art, have the particular advantages of possessing
 CC greater affinity for PTH, and in particular, are designed to have a novel
 CC recognition for amino acid residues extending beyond the first N-terminal
 CC PTH residue, and further have negligible cross-reactivity with the large
 CC non-molecular forms of PTH. PTH levels are an important parameter in
 CC patients suffering from hypercalcaemia, osteoporosis and primary
 CC hyperparathyroidism. The present sequence represents a PTH antigenic
 CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,
 CC canine and bovine PTH

XX
 SQ Sequence 11 AA;
 Query Match 82.0%; Score 50; DB 6; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 VSEIQFMHNG 12
 1 VSEIQFMHNG 11

Db
 RESULT 2
 AEG72608
 ID AEG72608 standard; peptide; 12 AA.
 XX
 AC AEG72608;
 XX
 DT 11-FEB-2003 (first entry)
 XX
 DE Parathyroid hormone antigenic peptide 1-12.
 XX
 KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
 KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Rattus sp.
 OS Bos taurus.
 OS Sus scrofa.
 OS Canis familiaris.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /label= Ser, Ala
 FT Misc-difference 7 /label= Leu, Phe
 FT
 XX US2002110871-A1.
 XX
 XX 15-AUG-2002.
 XX
 XX 05-DEC-2000; 2000US-00730174.
 XX
 XX 05-DEC-2000; 2000US-00730174.
 XX
 XX (ZARR/) ZARRADNIK R J.
 XX (LAVI/) LAVIGNE J R.
 XX
 XX Zahradnik RJ, Lavigne JR;
 PI

XX
 DR MPI; 2003-066685/06.
 XX
 PT New parathyroid hormone (PTH) antigenic peptide inducing the formation
 PT and isolation of antibodies having an affinity to it, useful for
 PT determining bioactive PTH levels in serum, plasma and/or cell culture
 PT media.
 XX
 PS Claim 2; Page 5; 11pp; English.

XX
 CC The invention relates to a new antigenic peptide for inducing the
 CC formation and isolation of antibodies having an affinity to it, being
 CC formed from the N-terminus of parathyroid hormone (PTH). Also included
 CC are: (1) a method for producing antibodies useful in the determination of
 CC PTH levels in a biological sample comprising: (a) providing at least one
 CC first peptide antigen comprising a peptide fragment of PTH; (b)
 CC administering the first peptide antigen to a host animal to induce
 CC antibody production; (c) monitoring the antibody titre produced; (d)
 CC isolating antisera produced in the host animal; and (e) selecting
 CC antisera from the isolated antisera produced in the host that is capable
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by
 CC the method; and (3) test kits and analytical procedures used for the
 CC determination of bioactive intact PTH utilising (ab). The method and
 CC compositions of the present invention are useful for determining
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
 CC The antigens, antibodies and methods of the present invention, as
 CC compared to prior art, have the particular advantages of possessing
 CC greater affinity for PTH, and in particular, are designed to have a novel
 CC recognition for amino acid residues extending beyond the first N-terminal
 CC PTH residue, and further have negligible cross-reactivity with the large
 CC non-molecular forms of PTH. PTH levels are an important parameter in
 CC patients suffering from hypercalcaemia, osteoporosis and primary
 CC hyperparathyroidism. The present sequence represents a PTH antigenic
 CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,
 CC canine and bovine PTH

XX
 SQ Sequence 12 AA;
 Query Match 82.0%; Score 50; DB 6; Length 12;
 Best Local Similarity 90.9%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 VSEIQFMHNG 12
 2 VSEIQFMHNG 12

Db
 RESULT 3
 AAY96968
 ID AAY96968 standard; peptide; 11 AA.
 XX
 AC AAY96968;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Parathyroid hormone N-terminal signaling domain (residues 1-11).
 XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
 KW bone reformation; resorption; remodeling; tetra-1; osteoporosis.
 XX
 OS Homo sapiens.
 XX
 XX WO200039278-A2.
 XX
 XX 06-JUL-2000.
 XX
 XX 30-DEC-1999; 99WO-US031108.
 XX
 XX 31-DEC-1998; 98US-0114577P.
 XX
 XX (GARD/) GARDELLA T J.
 XX (KRON/) KRONENBERG H M.
 XX (POTT/) POTTS J T.
 PA

PA (JUEP/) JUEPPNER H.
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
 XX WPI; 2000-452384/39.
 XX
 PT New compound comprising an amino terminal signaling functional domain
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for
 PT treating mammalian conditions characterized by decreases in bone mass.
 XX
 XX Claim 4; Page 92; 11pp; English.
 XX
 CC Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n
 CC -R are new. S is an amino terminal signaling functional domain of
 CC parathyroid hormone (PTH); L is a linker molecule present n times (where
 CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
 CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the
 CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
 CC sequence. The new compounds are used for treating mammalian conditions
 CC characterized by decreases in bone mass, determining rates of bone
 CC reformation, bone resorption and/or bone remodeling, treating diseases
 CC and disorders associated with decreased bone activity, increasing BMP
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
 CC non-peptide PTH (claimed). The new compound can be administered by
 CC inhalation unlike the large native PTH or PTHrp which avoids the need for
 CC regular injections to treat osteoporosis
 XX
 SQ Sequence 11 AA:
 QY
 Query Match 80.3%; Score 49; DB 3; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 AVSEIQFMHNL 11
 1 AVSEIQFMHNL 11
 RESULT 4
 AAR91644
 ID AAR91644 standard; peptide; 10 AA.
 XX
 AC AAR91644;
 XX
 DT 06-NOV-1996 (first entry)
 XX
 DE Human parathyroid hormone antigenic peptide hPTH 1-10.
 XX
 KM Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
 KM diagnosis; active hPTH 1-37.
 XX
 OS Synthetic.
 XX
 PN DE4434551-A1.
 XX
 PD 04-APR-1996.
 XX
 PF 28-SEP-1994; 94DE-04434551.
 XX
 PR 28-SEP-1994; 94DE-04434551.
 XX
 PA (FORSE/) FORSSMANN W.
 XX
 PI Adermann K, Forssmann W, Hock D, Meegerlein M;
 XX WPI; 1996-180391/19.
 XX
 PT New antigenic peptide(s) from human parathyroid hormone - and antibodies
 PT generated using them, able to distinguish between active and inactive
 PT forms of the hormone.
 XX
 PS Claim 2; Page 4; 5pp; German.
 XX

CC The present sequence is a specific example of claimed immunogenic
 CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
 CC terminal alpha-helical region and/or the non-structured region of the
 CC hormone. Antibodies and their binding fragments generated by injecting an
 CC animal with the peptides are useful as diagnostic reagents for
 CC determination of biologically active hPTH(1-37)
 XX
 SQ Sequence 10 AA:
 QY
 Query Match 68.3%; Score 42; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.37;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 AVSEIQFMHNL 10
 1 AVSEIQFMHNL 10
 RESULT 5
 AAY68767
 ID AAY68767 standard; peptide; 10 AA.
 XX
 AC AAY68767;
 XX
 DT 05-MAY-2000 (first entry)
 XX
 DE Amino acids 1-10 of a parathyroid hormone (PTH).
 XX
 KM Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;
 KM slimming treatment; cellulite; skin firming.
 XX
 OS Unidentified.
 XX
 PN WO200004047-A1.
 XX
 PD 27-JAN-2000.
 XX
 PF 07-JUL-1999; 99WO-FR001687.
 XX
 PR 17-JUL-1998; 98FR-00009193.
 XX
 PA (SEDE-) SEDERMA.
 XX
 PI Lintner K;
 XX
 DR WPI; 2000-171243/15.
 XX
 PT New parathyroid hormone fragment peptides, used as lipolysis stimulants
 PT in topically applied cosmetic compositions for slimming treatment of
 PT excessive weight in hips and thighs.
 XX
 PS Claim 1; Page 8; 16pp; French.
 XX
 CC The present sequence represents a parathyroid hormone (PTH) fragment,
 CC comprising amino acids 1-10. Parathyroid hormone fragments of the
 CC invention have lipolysis stimulating activity (especially when topically
 CC administered). The lipolytic activity of the peptides is enhanced when
 CC they are chemically modified to increase their lipophilicity. The
 CC peptides are used in cosmetic or dermatological compositions for skin
 CC care. They are especially used for slimming treatment of excessive weight
 CC in the thighs and hips, in the treatment of cellulite and for skin
 CC firming
 XX
 SQ Sequence 10 AA:
 QY
 Query Match 68.3%; Score 42; DB 3; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.37;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 AVSEIQFMHNL 10
 1 AVSEIQFMHNL 10

RESULT 6
 AAB86219 standard; peptide; 10 AA.
 XX
 AC AAB86219;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human parathyroid hormone immunogenic peptide SEQ ID 1.
 XX
 KM Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
 KM diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
 KM hypo-parathyroidism; hyper-parathyroidism.
 XX
 OS Homo sapiens.
 XX
 PN DE1961350-A1.
 XX
 PD 21-JUN-2001.
 XX
 PF 17-DEC-1999; 99DE-01061350.
 XX
 PR 17-DEC-1999; 99DE-01061350.
 XX
 PA (IMMU-) IMMUNDIAGNOSTIK AG.
 XX
 PI Armbruster FP;
 XX
 DR WPI; 2001-376318/40.
 XX
 PT Determining the content of physiologically active parathyroid hormone,
 PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
 PT reactive with different epitopes.
 XX
 PS Disclosure; Page 3; 10pp; German.
 XX
 CC This invention describes a novel method for determining (M1) the content
 CC of active parathyroid hormone (A) by treating a sample with (i) antibody
 CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
 CC and including the N-terminal residue and (ii) antibody (Ab2) that
 CC recognizes an epitope within the receptor-binding site of (A). The number
 CC of molecules that react with both antibodies is determined and used to
 CC calculate the content of physiologically active (A). The method is used
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that
 CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
 CC active and (ii) that apparently intact peptide may be biologically
 CC inactive, and also takes into account the fact that some fragments of (A)
 CC are antagonistic (these have the receptor-binding site but lack the N-
 CC terminus). It thus provides a true measure of the content of active
 CC physiologically active (A); contrast methods that measure intact peptide
 CC and its 1-37 fragment which may produce falsely high values. This
 CC sequence represents a peptide fragment used to illustrate the method of
 CC the invention
 XX
 SQ Sequence 10 AA;
 Query Match 68.9%; Score 42; DB 4; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.37;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DT 04-AUG-2003 (first entry)
 XX
 DE Human parathyroid hormone (hPTH) fragment (residues 1-10).
 XX
 KM Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;
 KM lipolysis; human; hPTH.
 XX
 OS Homo sapiens.
 XX
 PN WO2003035697-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 06-MAY-2002; 2002WO-KR000835.
 XX
 PR 27-SEP-2001; 2001KR-00060245.
 XX
 PR 15-MAR-2002; 2002KR-00014062.
 XX
 PA (GLDS) LG HOUSEHOLD & HEALTH CARE LTD.
 XX
 PI Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H,
 PI Chang M;
 XX
 DR WPI; 2003-468288/44.
 XX
 PT Novel fusion peptide comprising self cell-penetrating Tat peptide bound
 PT to human parathyroid hormone-derived peptide, useful as component of skin
 PT slimming cosmetic composition.
 XX
 PS Claim 5; Page 6; 32pp; English.
 XX
 CC The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-
 CC penetrating Tat peptide is bound to human parathyroid hormone-derived
 CC peptide (hPTHDP). The fusion peptide is useful as a component of skin
 CC slimming cosmetic composition. The fusion peptide does not cause
 CC irritation, easily and safely penetrates into integument and endothelium,
 CC does not cause skin disease and has superior lipolysis effects, and is
 CC durable. The present sequence represents a human parathyroid hormone
 CC (hPTH) fragment that can be used to construct the fusion peptide
 CC
 XX
 SQ Sequence 10 AA;
 Query Match 68.9%; Score 42; DB 6; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.37;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMEN 10
 :|||||
 DB 1 SVSEIQLMEN 10

RESULT 8
 AAY50600 standard; peptide; 11 AA.
 ID AAY50600
 XX
 AC AAY50600;
 XX
 DT 09-FEB-2000 (first entry)
 XX
 DE Resin bound cyclic peptide 33.
 XX
 KM Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;
 KM hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;
 KM osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;
 KM Cushing's syndrome; renal failure; hypertension; bone fracture repair.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH Misc-difference 1 /note= "FMOC-Ala"
 FT
 FT Misc-difference 3 /note= "Ser(OcBu)"
 FT

XX 22-OCT-1998; 98US-0105530P.
 XX (GARD/) GARDELLA T J.
 XX (KRON/) KRONENBERG H M.
 XX (POT/) POTTS J T.
 XX (JUEP/) JUEPNER H.
 XX Gardella TJ, Kronenberg HM, Potts JT, Juepner H;
 XX WPI: 2000-339693/29.
 XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
 XX acids that encode them, useful for treating osteoporosis.
 XX Disclosure; Page 26; 73pp; English.
 XX The invention relates to a novel parathyroid hormone (PTH) peptide
 XX (AAB01859) and parathyroid hormone-related peptide (PTHrP, AAB01860), and
 XX biologically active derivatives thereof (AAB01857-B01858, AAB01861-
 XX B01869). The peptides of the invention are at least 85% identical to the
 XX generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
 XX Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
 XX Met, Leu or Nle; X4 is Asp or Asn; X5 is Leu or Lys; X6 is His or Ser;
 XX provided that the peptide is not PTHrP(1-14). The peptides of the
 XX invention also encompass fragments of peptides of the invention
 XX consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
 XX terminal derivatives. PTH is a major regulator of calcium homeostasis,
 XX and is necessary for the normal function of the gastrointestinal,
 XX skeletal, neurological system, neuromuscular and cardiovascular systems.
 XX It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
 XX and to the recently identified PTH-2 receptor. PTH has a potent anabolic
 XX effect on the skeleton, and mediates calcium reabsorption, enhances
 XX phosphate clearance and vitamin D synthesis in the kidney. A homologous
 XX calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
 XX the renal and skeletal actions of PTH, and also bind to the PTH-1
 XX receptor. They do not bind to the PTH-2 receptor. The peptides of the
 XX invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
 XX AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
 XX B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
 XX osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
 XX medical disorders that arise from excessive or altered action of the PTH-
 XX 1/PTH-2 receptor. Detectably labeled peptides of the invention are also
 XX useful in the determination of rates of bone formation, bone resorption
 XX and/or bone remodeling in a patient. The peptides of the invention are
 XX "manipulated" versions of PTH or PTHrP which are delivered to a patient via
 XX non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
 XX PTH-1/PTH-2 receptor agonists
 XX
 XX Sequence 9 AA:
 XX
 XX Query Match 63.9%; Score 39; DB 3; Length 9;
 XX Best Local Similarity 88.9%; Pred. No. 1.4e+06;
 XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 1 AVSEIQFMH 9
 XX |||||
 XX 1 AVSEIQLMH 9
 XX
 XX RESULT 11
 XX ID AAY96966 standard; peptide; 9 AA.
 XX AC AAY96966;
 XX 31-OCT-2000 (first entry)
 XX Parathyroid hormone N-terminal signaling domain (residues 1-9).
 XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;

KW bone reformation; resorption; remodeling; telnet; osteoporosis.
 XX Homo sapiens.
 XX WO200039278-A2.
 XX 06-JUL-2000.
 XX 30-DEC-1999; 99WO-US031108.
 XX 31-DEC-1998; 98US-0114577P.
 XX (GARD/) GARDELLA T J.
 XX (KRON/) KRONENBERG H M.
 XX (POT/) POTTS J T.
 XX (JUEP/) JUEPNER H.
 XX Gardella TJ, Kronenberg HM, Potts JT, Juepner H;
 XX WPI: 2000-452384/39.
 XX New compound comprising an amino terminal signaling functional domain
 XX linked to a carboxy-terminal binding portion of parathyroid hormone for
 XX treating mammalian conditions characterized by decreases in bone mass.
 XX Claim 4; Page 92; 119pp; English.
 XX Compounds of the structure or formula S-(L)-n-B, R1-S-(L)-n-R or S-(L)-n
 XX -R, are new. S is an amino terminal signaling functional domain of
 XX parathyroid hormone (PTH); L is a linker molecule present n times (where
 XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
 XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the
 XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
 XX sequence. The new compounds are used for treating mammalian conditions
 XX characterized by decreases in bone mass, determining rates of bone
 XX reformation, bone resorption and/or bone remodeling, treating diseases
 XX and disorders associated with decreased bone activity, increasing BMP
 XX in a mammalian cell having PTH-1 receptors, or screening for a peptide or
 XX non-peptide PTH (claimed). The new compound can be administered by
 XX inhalation unlike the large native PTH or PTHrP which avoids the need for
 XX regular injections to treat osteoporosis
 XX
 XX Sequence 9 AA:
 XX
 XX Query Match 63.9%; Score 39; DB 3; Length 9;
 XX Best Local Similarity 88.9%; Pred. No. 1.4e+06;
 XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 1 AVSEIQFMH 9
 XX |||||
 XX 1 AVSEIQLMH 9
 XX
 XX RESULT 12
 XX ID AAR91645 standard; peptide; 9 AA.
 XX AC AAR91645;
 XX 06-NOV-1996 (first entry)
 XX Human parathyroid hormone antigenic peptide hPTH 1-9.
 XX Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
 XX diagnosis; active hPTH 1-37.
 XX Synthetic.
 XX DE4434551-A1.
 XX 04-APR-1996.
 XX 28-SEP-1994; 94DE-04434551.

XX 28-SEP-1994; 94DE-04434551.
PR (FORS/) FORSSMANN W.
XX
PI Adermann K, Forssmann W, Hock D, Maegerlein M;
XX WPI, 1996-180391/19.
DR
XX New antigenic peptide(s) from human parathyroid hormone - and antibodies
PT generated using them, able to distinguish between active and inactive
PT forms of the hormone.
XX
PS Claim 2, Page 4, 5pp; German.
XX
CC The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC terminal alpha-helical region and/or the non-structured region of the
CC hormone. Antibodies and their binding fragments generated by injecting an
CC animal with the peptides are useful as diagnostic reagents for
CC determination of biologically active hPTH(1-37)
XX
SQ Sequence 9 AA;
Query Match 59.0%; Score 36; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 AVSEIQFMH 9
DB 1 SVSEIQLMH 9
XX
RESULT 13
AAB01863
ID AAB01863 standard; peptide; 9 AA.
XX
AC AAB01863;
XX
DT 11-SEP-2000 (first entry)
XX
DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.
XX
KM Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KM calcium homeostasis; PTH-1 receptor; PTH-2; Vitamin D synthesis;
KM bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200023594-A1.
XX
PD 27-Apr-2000.
XX
PF 20-OCT-1999; 99WO-US024481.
XX
PR 22-OCT-1998; 98US-0105530P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI, 2000-339693/29.
XX
PT Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
PT acids that encode them, useful for treating osteoporosis.
XX
PS Disclosure; Page 26; 73pp; English.
XX
CC The invention relates to a novel parathyroid hormone (PTH) peptide

CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC B01869). The peptides of the invention are at least 85% identical to the
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC Gly-Iys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC provided that the peptide is not PTHrP(1-14). The peptides of the
CC invention also encompass fragments of peptides of the invention
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC and is necessary for the normal function of the gastrointestinal,
CC skeletal, neurological system, neuromuscular and cardiovascular systems.
CC It binds to both PTH-1 receptors on osteoclasts and renal tubular cells,
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC effect on the skeleton, and mediates calcium reabsorption, enhances
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous
CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC the renal and skeletal actions of PTH, and also bind to the PTH-1
CC receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC medical disorders that arise from excessive or altered action of the PTH-
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC useful in the determination of rates of bone formation, bone resorption
CC and/or bone remodeling in a patient. The peptides of the invention are
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC conventional synthetic chemistry, and can be delivered to a patient via
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC PTH-1/PTH-2 receptor agonists
XX
SQ Sequence 9 AA;
Query Match 59.0%; Score 36; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 AVSEIQFMH 9
DB 1 AVSEIQLMH 9
XX
RESULT 14
AAY96981
ID AAY96981 standard; peptide; 9 AA.
XX
AC AAY96981;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain.
XX
KM PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KM bone reformation; resorption; remodeling; tetracycl; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

```

XX DR WPI: 2000-452384/39.
XX
XX PT New compound comprising an amino terminal signaling functional domain
XX PT linked to a carboxy-terminal binding portion of parathyroid hormone for
XX PT treating mammalian conditions characterized by decreases in bone mass.
XX PS Claim 11; Page 33; 11pp; English.
XX
XX CC Compounds of the structure or formula S-(L)-n-R, R1-S-(L)-n-R or S-(L)-n
XX CC -R, are new. S is an amino terminal signaling functional domain of
XX CC parathyroid hormone (PTH); L is a linker molecule present n times (where
XX CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
XX CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the
XX CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
XX CC sequence. The new compounds are used for treating mammalian conditions
XX CC characterized by decreases in bone mass, determining rates of bone
XX CC reformation, bone resorption and/or bone remodeling, treating diseases
XX CC and disorders associated with decreased bone activity, increasing cAMP
XX CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
XX CC non-peptide PTH (claimed). The new compound can be administered by
XX CC inhalation unlike the large native PTH or PTHrP which avoids the need for
XX CC regular injections to treat osteoporosis
XX
XX SQ Sequence 9 AA:
XX
XX Query Match 59.0%; Score 36; DB 3; Length 9;
XX Best Local Similarity 77.8%; Pred. No. 1.4e+06;
XX Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 AYSEIQFMH 9
XX :|||||
XX 1 SVSEIQLMH 9
XX
XX
XX RESULT 15
XX AAB86220
XX ID AAB86220 standard; peptide; 9 AA.
XX
XX AC AAB86220;
XX
XX DT 03-SEP-2001 (first entry)
XX
XX DE Human parathyroid hormone immunogenic peptide SEQ ID 2.
XX
XX KM Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
XX KM diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
XX KM hypo-parathyroidism; hyper-parathyroidism.
XX
XX OS Homo sapiens.
XX
XX PN DE19961350-A1.
XX
XX PD 21-JUN-2001.
XX
XX PF 17-DEC-1999; 99DE-01061350.
XX
XX PR 17-DEC-1999; 99DE-01061350.
XX
XX PA (IMMU-) IMMUNDIAGNOSTIK AG.
XX
XX PI Ambruster FP.
XX
XX DR WPI: 2001-376318/40.
XX
XX PT Determining the content of physiologically active parathyroid hormone,
XX PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
XX PT reactive with different epitopes.
XX
XX PS Disclosure; Page 3; 10pp; German.
XX
XX CC This invention describes a novel method for determining (M1) the content
XX CC of active parathyroid hormone (A) by treating a sample with (1) antibody

```

```

CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (1) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyper-parathyroidism. The method (unlike known assays) recognizes that
CC (1) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (1) that apparently intact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention
XX
XX SQ Sequence 9 AA:
XX
XX Query Match 59.0%; Score 36; DB 4; Length 9;
XX Best Local Similarity 77.8%; Pred. No. 1.4e+06;
XX Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 AYSEIQFMH 9
XX :|||||
XX 1 SVSEIQLMH 9
XX
XX
XX Search completed: May 18, 2004, 10:01:54
XX Job time : 45.75 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 10:04:51 ; Search time 33.25 Seconds

(Without alignments)
100.425 Million cell updates/sec

Title: US-09-730-174A-6

Sequence: 1 AVSEIQFMNLG 12

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Gapop 10.0 , Gapext 0.5

Searched: 1145568 segs, 278261457 residues

Total number of hits satisfying chosen parameters: 166097

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Published Applications_AA.*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|-----------------------|-------------------|
| 1 | 61 | 100.0 | 12 9 US-09-730-174A-6 | Sequence 6, Appl1 |
| 2 | 58 | 95.1 | 12 9 US-09-730-174A-4 | Sequence 4, Appl1 |
| 3 | 57 | 93.4 | 11 9 US-09-730-174A-2 | Sequence 2, Appl1 |
| 4 | 55 | 90.2 | 12 9 US-09-730-174A-5 | Sequence 5, Appl1 |
| 5 | 52 | 85.2 | 12 9 US-09-730-174A-3 | Sequence 3, Appl1 |
| 6 | 51 | 83.6 | 11 9 US-09-730-174A-1 | Sequence 1, Appl1 |
| 7 | 42 | 68.9 | 10 14 US-10-168-185-1 | Sequence 7, Appl1 |
| 8 | 41 | 67.2 | 9 14 US-10-168-185-7 | Sequence 1, Appl1 |
| 9 | 39 | 63.9 | 9 14 US-10-192-673-6 | Sequence 6, Appl1 |
| 10 | 37 | 60.7 | 8 14 US-10-168-185-8 | Sequence 8, Appl1 |
| 11 | 36 | 59.0 | 9 14 US-10-192-673-7 | Sequence 7, Appl1 |
| 12 | 36 | 59.0 | 9 14 US-10-168-185-2 | Sequence 2, Appl1 |
| 13 | 29 | 47.5 | 9 14 US-10-192-673-8 | Sequence 8, Appl1 |
| 14 | 28 | 45.9 | 8 14 US-10-168-185-3 | Sequence 3, Appl1 |
| 15 | 27 | 44.3 | 10 14 US-10-233-187-8 | Sequence 8, Appl1 |

| | | | | |
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| 16 | 27 | 44.3 | 10 15 US-10-366-709-2 | Sequence 2, Appl1 |
| 17 | 26 | 42.6 | 9 14 US-10-192-673-10 | Sequence 10, Appl1 |
| 18 | 25 | 41.0 | 10 9 US-09-976-787-4 | Sequence 4, Appl1 |
| 19 | 25 | 41.0 | 10 9 US-09-865-198-4 | Sequence 4, Appl1 |
| 20 | 25 | 41.0 | 10 9 US-09-965-099-12 | Sequence 12, Appl1 |
| 21 | 25 | 41.0 | 10 10 US-09-563-222-41 | Sequence 41, Appl1 |
| 22 | 25 | 41.0 | 10 10 US-09-798-689-4 | Sequence 4, Appl1 |
| 23 | 25 | 41.0 | 10 12 US-10-339-656-19 | Sequence 19, Appl1 |
| 24 | 25 | 41.0 | 10 13 US-10-051-852-12 | Sequence 12, Appl1 |
| 25 | 25 | 41.0 | 10 14 US-10-195-752-108 | Sequence 108, Appl1 |
| 26 | 25 | 41.0 | 10 14 US-10-160-232-12 | Sequence 12, Appl1 |
| 27 | 25 | 41.0 | 10 14 US-10-160-232-18 | Sequence 18, Appl1 |
| 28 | 25 | 41.0 | 10 14 US-10-283-349-49 | Sequence 49, Appl1 |
| 29 | 25 | 41.0 | 10 14 US-10-230-880-115 | Sequence 115, Appl1 |
| 30 | 25 | 41.0 | 10 15 US-10-137-867-526 | Sequence 526, Appl1 |
| 31 | 25 | 41.0 | 10 15 US-10-366-709-3 | Sequence 3, Appl1 |
| 32 | 25 | 41.0 | 10 15 US-10-430-176-12 | Sequence 12, Appl1 |
| 33 | 25 | 41.0 | 11 11 US-09-791-551-13 | Sequence 13, Appl1 |
| 34 | 24 | 39.3 | 9 9 US-09-834-765-45 | Sequence 45, Appl1 |
| 35 | 24 | 39.3 | 9 9 US-09-834-765-55 | Sequence 55, Appl1 |
| 36 | 24 | 39.3 | 10 9 US-09-834-765-73 | Sequence 73, Appl1 |
| 37 | 24 | 39.3 | 10 9 US-09-834-765-78 | Sequence 78, Appl1 |
| 38 | 24 | 39.3 | 10 9 US-09-910-059-26 | Sequence 26, Appl1 |
| 39 | 24 | 39.3 | 10 14 US-10-033-741-61 | Sequence 61, Appl1 |
| 40 | 24 | 39.3 | 11 14 US-10-153-334-14 | Sequence 14, Appl1 |
| 41 | 24 | 39.3 | 12 14 US-10-319-130-16 | Sequence 16, Appl1 |
| 42 | 23 | 37.7 | 6 14 US-10-168-185-5 | Sequence 5, Appl1 |
| 43 | 23 | 37.7 | 7 14 US-10-168-185-4 | Sequence 4, Appl1 |
| 44 | 23 | 37.7 | 8 14 US-10-043-487-508 | Sequence 508, Appl1 |
| 45 | 23 | 37.7 | 9 14 US-10-147-140-26 | Sequence 26, Appl1 |

ALIGNMENTS

RESULT 1
US-09-730-174A-6
Sequence 6, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
FILE REFERENCE: IMMUNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 6
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-6
Query Match 100.0%; Score 61; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 AVSEIQFMNLG 12
1 AVSEIQFMNLG 12
RESULT 2
US-09-730-174A-4
Sequence 4, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
FILE REFERENCE: IMMUNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 4
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4

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; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4

Query Match
Best Local Similarity 95.1%; Score 58; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.00043;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQFMHNLG 12
Db 1 VSEIQFMHNLG 12

RESULT 3
US-09-730-174A-2
; Sequence 2, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMNE-001A
; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-2

Query Match
Best Local Similarity 93.4%; Score 57; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQFMHNLG 12
Db 1 VSEIQFMHNLG 11

RESULT 4
US-09-730-174A-5
; Sequence 5, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMNE-001A
; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5

Query Match
Best Local Similarity 90.2%; Score 55; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0015;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 AVSEIQFMHNLG 12
Db 1 AVSEIQFMHNLG 12

RESULT 5
US-09-730-174A-3
; Sequence 3, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMNE-001A
; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3

Query Match
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Best Local Similarity 83.3%; Pred. No. 0.0055;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMHNLG 12
Db 1 VSEIQFMHNLG 12

RESULT 6
US-09-730-174A-1
; Sequence 1, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; FILE REFERENCE: IMNE-001A
; CURRENT APPLICATION NUMBER: US/09/730.174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1

Query Match
Best Local Similarity 83.6%; Score 51; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQFMHNLG 12
Db 1 VSEIQFMHNLG 11

RESULT 7
US-10-166-185-1
; Sequence 1, Application US/10166185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Misbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
```


;; TITLE OF INVENTION: Activity in a Human Sample
;; FILE REFERENCE: HLZ-004US
;; CURRENT APPLICATION NUMBER: US/10/168,185
;; CURRENT FILING DATE: 2002-06-17
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911
;; PRIOR FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: DE 19961350
;; PRIOR FILING DATE: 1999-12-17
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-168-185-1

Query Match 68.9%; Score 42; DB 14; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.33;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 10
DB 1 VSEIQLMH 10

RESULT 8
US-10-168-185-7
;; Sequence 7, Application US/10168185
;; Publication No. US20030175802A1
;; GENERAL INFORMATION:
;; APPLICANT: Armbruster, Franz Paul
;; APPLICANT: Missbichler, Albert
;; APPLICANT: Schmidt-Gayk, Heinrich
;; APPLICANT: Roth, Heinz-Jürgen
;; TITLE OF INVENTION: Method for Determining Parathormone
;; FILE REFERENCE: HLZ-004US
;; CURRENT APPLICATION NUMBER: US/10/168,185
;; CURRENT FILING DATE: 2002-06-17
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911
;; PRIOR FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: DE 19961350
;; PRIOR FILING DATE: 1999-12-17
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 7
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-168-185-7

Query Match 67.2%; Score 41; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQFMH 10
DB 1 VSEIQLMH 9

RESULT 9
US-10-192-673-6
;; Sequence 6, Application US/10192673
;; Publication No. US20030166838A1
;; GENERAL INFORMATION:
;; APPLICANT: Gardella, Thomas J.
;; APPLICANT: Kronenberg, Henry
;; APPLICANT: Fotts, John T.
;; APPLICANT: Juppner, Harald
;; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;; FILE REFERENCE: 0609.4570002

;; CURRENT APPLICATION NUMBER: US/10/192,673
;; CURRENT FILING DATE: 2002-07-11
;; PRIOR APPLICATION NUMBER: U.S. 09/421,379
;; PRIOR FILING DATE: 1999-10-20
;; PRIOR APPLICATION NUMBER: U.S. 60/105,530
;; PRIOR FILING DATE: 1998-10-22
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
;; OTHER INFORMATION: peptide
US-10-192-673-6

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Best Local Similarity 88.9%; Pred. No. 1e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9
DB 1 AVSEIQLMH 9

RESULT 10
US-10-168-185-8
;; Sequence 8, Application US/10168185
;; Publication No. US20030175802A1
;; GENERAL INFORMATION:
;; APPLICANT: Armbruster, Franz Paul
;; APPLICANT: Missbichler, Albert
;; APPLICANT: Schmidt-Gayk, Heinrich
;; APPLICANT: Roth, Heinz-Jürgen
;; TITLE OF INVENTION: Method for Determining Parathormone
;; FILE REFERENCE: HLZ-004US
;; CURRENT APPLICATION NUMBER: US/10/168,185
;; CURRENT FILING DATE: 2002-06-17
;; PRIOR APPLICATION NUMBER: PCT/EP00/12911
;; PRIOR FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: DE 19961350
;; PRIOR FILING DATE: 1999-12-17
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-168-185-8

Query Match 60.7%; Score 37; DB 14; Length 8;
Best Local Similarity 87.5%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SEIQFMH 10
DB 1 SEIQLMH 8

RESULT 11
US-10-192-673-7
;; Sequence 7, Application US/10192673
;; Publication No. US20030166838A1
;; GENERAL INFORMATION:
;; APPLICANT: Gardella, Thomas J.
;; APPLICANT: Kronenberg, Henry
;; APPLICANT: Fotts, John T.
;; APPLICANT: Juppner, Harald
;; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)

FILE REFERENCE: 0609.4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-10-192-673-7

Query Match 59.0%; Score 36; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQPMH 9
DB 1 AVSEIQLH 9

RESULT 12
US-10-168-185-2
Sequence 2, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Urgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-185-2

Query Match 59.0%; Score 36; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQPMH 9
DB 1 SVSEIQLM 9

RESULT 13
US-10-192-673-8
Sequence 8, Application US/10192673
Publication No. US2003016838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of Parathyroid Hormone (PTH) and Parathyroid

TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
FILE REFERENCE: 0609.4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-10-192-673-8

Query Match 47.5%; Score 29; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIQPMH 9
DB 1 AVSEIQLH 9

RESULT 14
US-10-168-185-3
Sequence 3, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Urgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-185-3

Query Match 45.9%; Score 28; DB 14; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQPMH 8
DB 1 SVSEIQLM 8

RESULT 15
US-10-232-187-8
Sequence 8, Application US/10232187
Publication No. US20030092091A1
GENERAL INFORMATION:
APPLICANT: Abrahamson, Julie A.
APPLICANT: Bochner, Bruce
APPLICANT: Erickson-Miller, Connie L.
APPLICANT: Kikly, Kristine K.
APPLICANT: Schleimer, Robert

Tue May 18 12:03:11 2004

us-09-730-174a-6.closed.rapb

Page 5

APPLICANT: Nalku, Turkan E.
TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies
FILE REFERENCE: GH50042-1
CURRENT APPLICATION NUMBER: US/10/232,187
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/187,595
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: PCT/US01/07193
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/315,943
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 60/349,830
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 60/394,741
PRIOR FILING DATE: 2002-07-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapien
US-10-232-187-8

Query Match 44.3%; Score 27; DB 14; Length 10;
Best Local Similarity 44.4%; Pred. No. 2e+02; 3; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIOFMH 9
| : : |
Db 2 ATSSVSVMH 10

Search completed: May 18, 2004, 10:21:00
Job time : 33.25 secs

Tue May 18 12:03:11 2004

us-09-730-174a-6.closed.ra1

Page 1

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CM protein - protein search, using sw model

Run on: May 18, 2004, 09:58:45 ; Search time 12.75 Seconds
(without alignments)
48.589 Million cell updates/sec

Title: US-09-730-174A-6
Perfect score: 61
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/2/1aa/PTCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|-------------------------|--------------------|
| 1 | 49 | 80.3 | 12 4 US-09-442-989-31 | Sequence 31, Appl |
| 2 | 42 | 68.9 | 10 3 US-08-817-547A-1 | Sequence 1, Appl |
| 3 | 39 | 63.9 | 9 4 US-09-421-379-6 | Sequence 6, Appl |
| 4 | 36 | 59.0 | 9 3 US-08-817-547A-2 | Sequence 2, Appl |
| 5 | 31 | 50.8 | 9 4 US-09-421-379-7 | Sequence 7, Appl |
| 6 | 31 | 50.8 | 11 6 5460978-3 | Patent No. 5460978 |
| 7 | 29 | 47.5 | 9 4 US-09-421-379-8 | Sequence 8, Appl |
| 8 | 29 | 47.5 | 12 2 US-08-140-137A-42 | Sequence 42, Appl |
| 9 | 28 | 45.9 | 8 3 US-08-817-547A-3 | Sequence 3, Appl |
| 10 | 27 | 44.3 | 12 2 US-08-482-228-42 | Sequence 42, Appl |
| 11 | 27 | 44.3 | 12 3 US-08-482-528-42 | Sequence 42, Appl |
| 12 | 26 | 42.6 | 9 4 US-09-421-379-10 | Sequence 10, Appl |
| 13 | 25 | 41.0 | 10 2 US-08-116-778E-9 | Sequence 9, Appl |
| 14 | 25 | 41.0 | 10 2 US-08-438-562-9 | Sequence 9, Appl |
| 15 | 25 | 41.0 | 10 2 US-08-483-528B-97 | Sequence 97, Appl |
| 16 | 25 | 41.0 | 10 3 US-08-783-853A-12 | Sequence 12, Appl |
| 17 | 25 | 41.0 | 10 3 US-08-836-561-49 | Sequence 49, Appl |
| 18 | 25 | 41.0 | 10 3 US-09-280-028-12 | Sequence 12, Appl |
| 19 | 25 | 41.0 | 10 4 US-09-344-050-12 | Sequence 12, Appl |
| 20 | 25 | 41.0 | 10 4 US-09-393-385B-108 | Sequence 108, Appl |
| 21 | 25 | 41.0 | 10 4 US-09-434-122-49 | Sequence 49, Appl |
| 22 | 25 | 41.0 | 10 4 US-09-091-071-3 | Sequence 3, Appl |
| 23 | 24 | 39.3 | 5 2 US-08-177-109A-56 | Sequence 56, Appl |
| 24 | 24 | 39.3 | 5 2 US-08-687-706-56 | Sequence 56, Appl |
| 25 | 24 | 39.3 | 5 2 US-08-817-547A-17 | Sequence 17, Appl |
| 26 | 24 | 39.3 | 5 2 US-08-817-547A-16 | Sequence 16, Appl |
| 27 | 24 | 39.3 | 7 3 US-08-817-547A-15 | Sequence 15, Appl |

| | | | | |
|----|----|------|-----------------------|-------------------|
| 28 | 24 | 39.3 | 8 2 US-08-748-021-64 | Sequence 64, Appl |
| 29 | 24 | 39.3 | 8 3 US-08-817-547A-14 | Sequence 14, Appl |
| 30 | 24 | 39.3 | 8 3 US-08-974-297-64 | Sequence 64, Appl |
| 31 | 24 | 39.3 | 9 3 US-08-817-547A-13 | Sequence 13, Appl |
| 32 | 24 | 39.3 | 10 3 US-08-432-694-5 | Sequence 5, Appl |
| 33 | 24 | 39.3 | 10 3 US-08-817-547A-7 | Sequence 7, Appl |
| 34 | 24 | 39.3 | 10 3 US-09-171-945-26 | Sequence 26, Appl |
| 35 | 24 | 39.3 | 11 1 US-08-432-694-3 | Sequence 3, Appl |
| 36 | 23 | 37.7 | 6 3 US-08-817-547A-5 | Sequence 5, Appl |
| 37 | 23 | 37.7 | 7 3 US-08-817-547A-4 | Sequence 4, Appl |
| 38 | 23 | 37.7 | 9 1 US-07-822-043-26 | Sequence 26, Appl |
| 39 | 23 | 37.7 | 9 1 US-08-346-455B-26 | Sequence 26, Appl |
| 40 | 23 | 37.7 | 9 3 US-08-977-221-26 | Sequence 26, Appl |
| 41 | 23 | 37.7 | 9 4 US-09-483-831B-26 | Sequence 26, Appl |
| 42 | 23 | 37.7 | 9 5 PCT-US95-06613-26 | Sequence 26, Appl |
| 43 | 23 | 37.7 | 10 4 US-09-771-415-3 | Sequence 3, Appl |
| 44 | 23 | 37.7 | 12 3 US-09-064-750-1 | Sequence 1, Appl |
| 45 | 22 | 36.1 | 10 1 US-08-615-181-83 | Sequence 83, Appl |

ALIGNMENTS

RESULT 1
US-09-442-989-31
Sequence 31, Application US/09442989
Patent No. 6569993
GENERAL INFORMATION:
APPLICANT: Siedeski, Adam W.
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
FILE REFERENCE: A3113B-US
CURRENT APPLICATION NUMBER: US/09/442,989
CURRENT FILING DATE: 1999-11-18
EARLIER APPLICATION NUMBER: 60/081,897
EARLIER FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)
OTHER INFORMATION: FMOC-Ala
NAME/KEY: PEPTIDE
LOCATION: (3)
OTHER INFORMATION: Ser(OcBu)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (4)
OTHER INFORMATION: Glu(OcBu)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (6)
OTHER INFORMATION: Glu(Trt)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (9)
OTHER INFORMATION: His(Trt)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (10)
OTHER INFORMATION: Asn(Trt)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: Nle
US-09-442-989-31

Tue May 18 12:03:11 2004

us-09-730-174a-6.closed.ra1

Page 2

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Query Match      80.3%; Score 49; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AVSEIOFMNLG 12
      1 AVSEIOQLXNHLG 12

Db

RESULT 2
US-08-817-547A-1
; Sequence 1, Application US/08817547A
; Patent No. 6030790
; GENERAL INFORMATION:
; APPLICANT: Ademann, Knut
; APPLICANT: Hock, Dieter
; APPLICANT: Magerlein, Markus
; TITLE OF INVENTION: Peptides from the hPTH Sequence
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,547A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03757
; FILING DATE: 29 SEPT 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FROST, ROGER T.
; REGISTRATION NUMBER: 22,176
; REFERENCE/DOCKET NUMBER: 07826-0007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: no
; ANTI-SENSE: no
US-08-817-547A-1

Query Match      68.9%; Score 42; DB 3; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.06;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 AVSEIOFMNH 10
      1 SVSEIOQLMNH 10

Db

RESULT 3
US-09-421-379-6
; Sequence 6, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kironberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
```

```
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)
; FILE REFERENCE: 0609.4570001
; CURRENT APPLICATION NUMBER: US/09/421,379
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: U.S. 60/105,530
; EARLIER FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-421-379-6

Query Match      63.9%; Score 39; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AVSEIOFMH 9
      1 AVSEIOQLMH 9

Db

RESULT 4
US-08-817-547A-2
; Sequence 2, Application US/08817547A
; Patent No. 6030790
; GENERAL INFORMATION:
; APPLICANT: Ademann, Knut
; APPLICANT: Hock, Dieter
; APPLICANT: Magerlein, Markus
; TITLE OF INVENTION: Peptides from the hPTH Sequence
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,547A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03757
; FILING DATE: 29 SEPT 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FROST, ROGER T.
; REGISTRATION NUMBER: 22,176
; REFERENCE/DOCKET NUMBER: 07826-0007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: no
; ANTI-SENSE: no
US-08-817-547A-2
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Query Match 59.0%; Score 36; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9
Db 1 SVSEIQLMH 9

RESULT 5
US-09-421-379-7
Sequence 7, Application US/09421379
Patent No. 6495662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
FILE REFERENCE: 0609.4570001
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-7

Query Match 59.0%; Score 36; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9
Db 1 AVSEIQLMH 9

RESULT 6
5460978-3
Patent No. 5460978
APPLICANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,
BRUCE E.; WETTENHALL, RICHARD E.H.
TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL
HYPERCALCEMIA OF MALIGNANCY-PTHrP
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/715,280
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 199,235
FILING DATE: 09-MAY-1988
APPLICATION NUMBER:
FILING DATE:
SEQ ID NO:3
LENGTH: 11
5460978-3

Query Match 50.8%; Score 31; DB 6; Length 11;
Best Local Similarity 70.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 10

Db 1 AVSEHQLMH 10

RESULT 7
US-09-421-379-8
Sequence 8, Application US/09421379
Patent No. 6495662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
FILE REFERENCE: 0609.4570001
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-8

Query Match 47.5%; Score 29; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9
Db 1 AVSEHQLMH 9

RESULT 8
US-08-140-137A-42
Sequence 42, Application US/08140137A
Patent No. 5817617
GENERAL INFORMATION:
APPLICANT: TUOMANEN, ELAINE
APPLICANT: MASURE, H. R.
TITLE OF INVENTION: ANALOGS OF ENDOTHELIAL LEUKOCYTE
ADHESION MOLECULE (ELAM)
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/140,137A
FILING DATE: 27-MAY-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-096
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684

TELEX: 133521
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: Card peptide sequence
US-08-140-137A-42

Query Match 47.5%; Score 29; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQFMH 9
DB 5 ISEECFVH 12

RESULT 9
US-08-817-547A-3
Sequence 3, Application US/08817547A
Patent No. 6030790
GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: no
ANTI-SENSE: no
US-08-817-547A-3

Query Match 45.9%; Score 28; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 8
DB 1 SVSEIQFMH 8

RESULT 10
US-08-482-228-42
Sequence 42, Application US/08482228
Patent No. 5968753
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,228
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-228-42

Query Match 44.3%; Score 27; DB 2; Length 12;
Best Local Similarity 55.6%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9
DB 3 ASSSVTFMH 11

RESULT 11
US-08-482-528-42
Sequence 42, Application US/08482528
Patent No. 6017719
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine

STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,528
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthe, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-528-42

Query Match 44.3%; Score 27; DB 3; Length 12;
Best Local Similarity 55.6%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9
DB 3 ASSSVTFMH 11

RESULT 12
US-09-421-379-10
Sequence 10, Application US/09421379
Patent No. 6495662
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)
FILE REFERENCE: 0609.4570001
CURRENT APPLICATION NUMBER: US/09/421,379
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 9
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-09-421-379-10

Query Match 42.6%; Score 26; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 3e+05;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9
DB 1 SVSEHQLH 9

RESULT 13
US-08-116-778E-9
Sequence 9, Application US/08116778E
Patent No. 5830470
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KIWANA, YOSHITAKA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 243-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-778E-9

Query Match 41.0%; Score 25; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9
DB 2 ASSSVTFMH 10

RESULT 14
US-08-438-562-9
Sequence 9, Application US/08438562
Patent No. 5874255
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KIWANA, YOSHITAKA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY T.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-438-562-9

Query Match 41.0%; Score 25; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIOFMH 9
Db 2 ASSSVSYMH 10

RESULT 15
US-08-483-5288-97
Sequence 97, Application US/084835288
Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUMANA, YOSHIOHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-5288-97

Query Match 41.0%; Score 25; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIOFMH 9
Db 2 ASSSVSYMH 10

Search completed: May 18, 2004, 10:06:44
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